

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: EPELBAUM, SABINE URSULA  
FALCO, SAVERIO CARL  
MCDEVITT, RAYMOND ERVIN, III
- (ii) TITLE OF INVENTION: CHIMERIC GENES AND METHODS FOR  
INCREASING THE LYSINE CONTENT OF  
THE SEEDS OF PLANTS
- (iii) NUMBER OF SEQUENCES: 132
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
  - (B) STREET: 1007 MARKET STREET
  - (C) CITY: WILMINGTON
  - (D) STATE: DELAWARE
  - (E) COUNTRY: U.S.A.
  - (F) ZIP: 19898
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: DISKETTE, 3.50 INCH
  - (B) COMPUTER: IBM PC COMPATIBLE
  - (C) OPERATING SYSTEM: MICROSOFT OFFICE 97
  - (D) SOFTWARE: MICROSOFT WINDOWS 95
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE:
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: 08/824,627
  - (B) FILING DATE: MARCH 27, 1997
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: CHRISTENBURY, LYNNE M.
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  - (C) REFERENCE/DOCKET NUMBER: BB-1037-F
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: 302-992-5481
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  - (C) TELEX: 835420

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1350 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1350

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATG GCT GAA ATT GTT GTC TCC AAA TTT GGC GGT ACC AGC GTA GCT GAT	48
Met Ala Glu Ile Val Val Ser Lys Phe Gly Gly Thr Ser Val Ala Asp	
1 5 10 15	
TTT GAC GCC ATG AAC CGC AGC GCT GAT ATT GTG CTT TCT GAT GCC AAC	96
Phe Asp Ala Met Asn Arg Ser Ala Asp Ile Val Leu Ser Asp Ala Asn	
20 25 30	
GTG CGT TTA GTT GTC CTC TCG GCT TCT GCT GGT ATC ACT AAT CTG CTG	144
Val Arg Leu Val Val Leu Ser Ala Ser Ala Gly Ile Thr Asn Leu Leu	
35 40 45	
GTC GCT TTA GCT GAA GGA CTG GAA CCT GGC GAG CGA TTC GAA AAA CTC	192
Val Ala Leu Ala Glu Gly Leu Glu Pro Gly Glu Arg Phe Glu Lys Leu	
50 55 60	
GAC GCT ATC CGC AAC ATC CAG TTT GCC ATT CTG GAA CGT CTG CGT TAC	240
Asp Ala Ile Arg Asn Ile Gln Phe Ala Ile Leu Glu Arg Leu Arg Tyr	
65 70 75 80	
CCG AAC GTT ATC CGT GAA GAG ATT GAA CGT CTG CTG GAG AAC ATT ACT	288
Pro Asn Val Ile Arg Glu Glu Ile Glu Arg Leu Leu Glu Asn Ile Thr	
85 90 95	
GTT CTG GCA GAA GCG GCG GCG CTG GCA ACG TCT CCG GCG CTG ACA GAT	336
Val Leu Ala Glu Ala Ala Ala Leu Ala Thr Ser Pro Ala Leu Thr Asp	
100 105 110	
GAG CTG GTC AGC CAC GGC GAG CTG ATG TCG ACC CTG CTG TTT GTT GAG	384
Glu Leu Val Ser His Gly Glu Leu Met Ser Thr Leu Leu Phe Val Glu	
115 120 125	
ATC CTG CGC GAA CGC GAT GTT CAG GCA CAG TGG TTT GAT GTA CGT AAA	432
Ile Leu Arg Glu Arg Asp Val Gln Ala Gln Trp Phe Asp Val Arg Lys	
130 135 140	
GTG ATG CGT ACC AAC GAC CGA TTT GGT CGT GCA GAG CCA GAT ATA GCC	480
Val Met Arg Thr Asn Asp Arg Phe Gly Arg Ala Glu Pro Asp Ile Ala	
145 150 155 160	

GCG CTG GCG GAA CTG GCC GCG CTG CAG CTG CTC CCA CGT CTC AAT GAA	528
Ala Leu Ala Glu Leu Ala Ala Leu Gln Leu Leu Pro Arg Leu Asn Glu	
165 170 175	
GGC TTA GTG ATC ACC CAG GGA TTT ATC GGT AGC GAA AAT AAA GGT CGT	576
Gly Leu Val Ile Thr Gln Gly Phe Ile Gly Ser Glu Asn Lys Gly Arg	
180 185 190	
ACA ACG ACG CTT GGC CGT GGA GGC AGC GAT TAT ACG GCA GCC TTG CTG	624
Thr Thr Thr Leu Gly Arg Gly Gly Ser Asp Tyr Thr Ala Ala Leu Leu	
195 200 205	
GCG GAG GCT TTA CAC GCA TCT CGT GTT GAT ATC TGG ACC GAC GTC CCG	672
Ala Glu Ala Leu His Ala Ser Arg Val Asp Ile Trp Thr Asp Val Pro	
210 215 220	
GGC ATC TAC ACC ACC GAT CCA CGC GTA GTT TCC GCA GCA AAA CGC ATT	720
Gly Ile Tyr Thr Thr Asp Pro Arg Val Val Ser Ala Ala Lys Arg Ile	
225 230 235 240	
GAT GAA ATC GCG TTT GCC GAA GCG GCA GAG ATG GCA ACT TTT GGT GCA	768
Asp Glu Ile Ala Phe Ala Glu Ala Ala Glu Met Ala Thr Phe Gly Ala	
245 250 255	
AAA GTA CTG CAT CCG GCA ACG TTG CTA CCC GCA GTA CGC AGC GAT ATC	816
Lys Val Leu His Pro Ala Thr Leu Leu Pro Ala Val Arg Ser Asp Ile	
260 265 270	
CCG GTC TTT GTC GGC TCC AGC AAA GAC CCA CGC GCA GGT GGT ACG CTG	864
Pro Val Phe Val Gly Ser Ser Lys Asp Pro Arg Ala Gly Gly Thr Leu	
275 280 285	
GTG TGC AAT AAA ACT GAA AAT CCG CCG CTG TTC CGC GCT CTG GCG CTT	912
Val Cys Asn Lys Thr Glu Asn Pro Pro Leu Phe Arg Ala Leu Ala Leu	
290 295 300	
CGT CGC AAT CAG ACT CTG CTC ACT TTG CAC AGC CTG AAT ATG CTG CAT	960
Arg Arg Asn Gln Thr Leu Leu Thr Leu His Ser Leu Asn Met Leu His	
305 310 315 320	
TCT CGC GGT TTC CTC GCG GAA GTT TTC GGC ATC CTC GCG CGG CAT AAT	1008
Ser Arg Gly Phe Leu Ala Glu Val Phe Gly Ile Leu Ala Arg His Asn	
325 330 335	
ATT TCG GTA GAC TTA ATC ACC ACG TCA GAA GTG AGC GTG GCA TTA ACC	1056
Ile Ser Val Asp Leu Ile Thr Thr Ser Glu Val Ser Val Ala Leu Thr	
340 345 350	
CTT GAT ACC ACC GGT TCA ACC TCC ACT GGC GAT ACG TTG CTG ACG CAA	1104
Leu Asp Thr Thr Gly Ser Thr Ser Thr Gly Asp Thr Leu Leu Thr Gln	
355 360 365	
TCT CTG CTG ATG GAG CTT TCC GCA CTG TGT CGG GTG GAG GTG GAA GAA	1152
Ser Leu Leu Met Glu Leu Ser Ala Leu Cys Arg Val Glu Val Glu Glu	
370 375 380	

GGT	CTG	GCG	CTG	GTC	GCG	TTG	ATT	GGC	AAT	GAC	CTG	TCA	AAA	GCC	TGC	1200
Gly	Leu	Ala	Leu	Val	Ala	Leu	Ile	Gly	Asn	Asp	Leu	Ser	Lys	Ala	Cys	
385					390				395						400	
GCC	GTT	GGC	AAA	GAG	GTA	TTC	GGC	GTA	CTG	GAA	CCG	TTC	AAC	ATT	CGC	1248
Ala	Val	Gly	Lys	Glu	Val	Phe	Gly	Val	Leu	Glu	Pro	Phe	Asn	Ile	Arg	
				405					410						415	
ATG	ATT	TGT	TAT	GGC	GCA	TCC	AGC	CAT	AAC	CTG	TGC	TTC	CTG	GTG	CCC	1296
Met	Ile	Cys	Tyr	Gly	Ala	Ser	Ser	His	Asn	Leu	Cys	Phe	Leu	Val	Pro	
			420					425							430	
GGC	GAA	GAT	GCC	GAG	CAG	GTG	GTG	CAA	AAA	CTG	CAT	AGT	AAT	TTG	TTT	1344
Gly	Glu	Asp	Ala	Glu	Gln	Val	Val	Gln	Lys	Leu	His	Ser	Asn	Leu	Phe	
		435						440							445	
GAG	TAA															1350
Glu	*															
		450														

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GATCCATGGC TGAAATTGTT GTCTCCAAAT TTGGCG 36

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GTACCGCCAA ATTTGGAGAC AACAAATTCA GCCATG 36

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 48 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CCCGGGCCAT GGCTACAGGT TTAACAGCTA AGACCGGAGT AGAGCACT

48

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GATATCGAAT TCTCATTATA GAACTCCAGC TTTTTC

37

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 917 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 3..911

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CC ATG GCT ACA GGT TTA ACA GCT AAG ACC GGA GTA GAG CAC TTC GGC	47
Met Ala Thr Gly Leu Thr Ala Lys Thr Gly Val Glu His Phe Gly	
1 5 10 15	
ACC GTT GGA GTA GCA ATG GTT ACT CCA TTC ACG GAA TCC GGA GAC ATC	95
Thr Val Gly Val Ala Met Val Thr Pro Phe Thr Glu Ser Gly Asp Ile	
20 25 30	
GAT ATC GCT GCT GGC CGC GAA GTC GCG GCT TAT TTG GTT GAT AAG GGC	143
Asp Ile Ala Ala Gly Arg Glu Val Ala Ala Tyr Leu Val Asp Lys Gly	
35 40 45	
TTG GAT TCT TTG GTT CTC GCG GGC ACC ACT GGT GAA TCC CCA ACG ACA	191
Leu Asp Ser Leu Val Leu Ala Gly Thr Thr Gly Glu Ser Pro Thr Thr	
50 55 60	
ACC GCC GCT GAA AAA CTA GAA CTG CTC AAG GCC GTT CGT GAG GAA GTT	239
Thr Ala Ala Glu Lys Leu Glu Leu Leu Lys Ala Val Arg Glu Glu Val	
65 70 75	
GGG GAT CGG GCG AAG CTC ATC GCC GGT GTC GGA ACC AAC AAC ACG CGG	287
Gly Asp Arg Ala Lys Leu Ile Ala Gly Val Gly Thr Asn Asn Thr Arg	
80 85 90 95	

ACA	TCT	GTG	GAA	CTT	GCG	GAA	GCT	GCT	GCT	TCT	GCT	GGC	GCA	GAC	GGC	335
Thr	Ser	Val	Glu	Leu	Ala	Glu	Ala	Ala	Ala	Ser	Ala	Gly	Ala	Asp	Gly	
			100						105					110		
CTT	TTA	GTT	GTA	ACT	CCT	TAT	TAC	TCC	AAG	CCG	AGC	CAA	GAG	GGA	TTG	383
Leu	Leu	Val	Val	Thr	Pro	Tyr	Tyr	Ser	Lys	Pro	Ser	Gln	Glu	Gly	Leu	
			115					120					125			
CTG	GCG	CAC	TTC	GGT	GCA	ATT	GCT	GCA	GCA	ACA	GAG	GTT	CCA	ATT	TGT	431
Leu	Ala	His	Phe	Gly	Ala	Ile	Ala	Ala	Ala	Thr	Glu	Val	Pro	Ile	Cys	
		130					135					140				
CTC	TAT	GAC	ATT	CCT	GGT	CGG	TCA	GGT	ATT	CCA	ATT	GAG	TCT	GAT	ACC	479
Leu	Tyr	Asp	Ile	Pro	Gly	Arg	Ser	Gly	Ile	Pro	Ile	Glu	Ser	Asp	Thr	
	145					150				155						
ATG	AGA	CGC	CTG	AGT	GAA	TTA	CCT	ACG	ATT	TTG	GCG	GTC	AAG	GAC	GCC	527
Met	Arg	Arg	Leu	Ser	Glu	Leu	Pro	Thr	Ile	Leu	Ala	Val	Lys	Asp	Ala	
160					165				170					175		
AAG	GGT	GAC	CTC	GTT	GCA	GCC	ACG	TCA	TTG	ATC	AAA	GAA	ACG	GGA	CTT	575
Lys	Gly	Asp	Leu	Val	Ala	Ala	Thr	Ser	Leu	Ile	Lys	Glu	Thr	Gly	Leu	
			180					185						190		
GCC	TGG	TAT	TCA	GGC	GAT	GAC	CCA	CTA	AAC	CTT	GTT	TGG	CTT	GCT	TTG	623
Ala	Trp	Tyr	Ser	Gly	Asp	Asp	Pro	Leu	Asn	Leu	Val	Trp	Leu	Ala	Leu	
			195					200					205			
GGC	GGA	TCA	GGT	TTC	ATT	TCC	GTA	ATT	GGA	CAT	GCA	GCC	CCC	ACA	GCA	671
Gly	Gly	Ser	Gly	Phe	Ile	Ser	Val	Ile	Gly	His	Ala	Ala	Pro	Thr	Ala	
		210					215					220				
TTA	CGT	GAG	TTG	TAC	ACA	AGC	TTC	GAG	GAA	GGC	GAC	CTC	GTC	CGT	GCG	719
Leu	Arg	Glu	Leu	Tyr	Thr	Ser	Phe	Glu	Glu	Gly	Asp	Leu	Val	Arg	Ala	
	225					230					235					
CGG	GAA	ATC	AAC	GCC	AAA	CTA	TCA	CCG	CTG	GTA	GCT	GCC	CAA	GGT	CGC	767
Arg	Glu	Ile	Asn	Ala	Lys	Leu	Ser	Pro	Leu	Val	Ala	Ala	Gln	Gly	Arg	
240					245				250					255		
TTG	GGT	GGA	GTC	AGC	TTG	GCA	AAA	GCT	GCT	CTG	CGT	CTG	CAG	GGC	ATC	815
Leu	Gly	Gly	Val	Ser	Leu	Ala	Lys	Ala	Ala	Leu	Arg	Leu	Gln	Gly	Ile	
			260					265					270			
AAC	GTA	GGA	GAT	CCT	CGA	CTT	CCA	ATT	ATG	GCT	CCA	AAT	GAG	CAG	GAA	863
Asn	Val	Gly	Asp	Pro	Arg	Leu	Pro	Ile	Met	Ala	Pro	Asn	Glu	Gln	Glu	
			275				280					285				
CTT	GAG	GCT	CTC	CGA	GAA	GAC	ATG	AAA	AAA	GCT	GGA	GTT	CTA	TAA	TGAGAATTC	917
Leu	Glu	Ala	Leu	Arg	Glu	Asp	Met	Lys	Lys	Ala	Gly	Val	Leu	*		
	290					295					300					

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CTTCCCGTGA CCAATGGGCCA TC

22

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 75 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CATGGCTGGC TTCCCCACGA GGAAGACCAA CAATGACATT ACCTCCATTG CTAGCAACGG 60

TGGAAGAGTA CAATG

75

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 75 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CATGCATTGT ACTCTTCCAC CGTTGCTAGC AATGGAGGTA ATGTCATTGT TGGTCTTCCT 60

CGTGGGGAAG CCAGC

75

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 90 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CATGGCTTCC TCAATGATCT CCTCCCCAGC TGTTACCACC GTCAACCGTG CCGGTGCCGG 60

CATGGTTGCT CCATTACCG GCCTCAAAAG

90

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 90 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CATGCTTTTG AGGCCGGTGA ATGGAGCAAC CATGCCGGCA CCGGCACGGT TGACGGTGGT 60  
AACAGCTGGG GAGGAGATCA TTGAGGAAGC 90

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CCGGTTTGCT GTAATAGGTA CCA 23

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 31 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AGCTTGGTAC CTATTACAGC AAACCGGCAT G 31

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GCTTCCTCAA TGATCTCCTC CCCAGCT 27



(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 28 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CATTGTACTC TTCCACCGTT GCTAGCAA

28

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION: 1..20
  - (D) OTHER INFORMATION: /product= "synthetic  
oligonucleotide"  
/standard\_name= "SM  
70"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CTGACTCGCT GCGCTCGGTC

20

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION: 1..24
  - (D) OTHER INFORMATION: /product= "synthetic  
oligonucleotide"  
/standard\_name= "SM  
71"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

TATTTTCTCC TTACGCATCT GTGC

24

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION: 1..27
  - (D) OTHER INFORMATION: /product= "synthetic  
oligonucleotide"  
/standard\_name= "SM  
78"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TTCATCGATA GGCGACCACA CCCGTCC

27

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION: 1..27
  - (D) OTHER INFORMATION: /product= "synthetic  
oligonucleotide"  
/standard\_name= "SM  
79"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

AATATCGATG CCACGATGCG TCCGGCG

27

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 55 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION: 1..55

(D) OTHER INFORMATION: /product= "synthetic  
oligonucleotide"  
/standard\_name= "SM  
81"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CATGGAGGAG AAGATGAAGG CGATGGAAGA GAAGATGAAG GCGTGATAGG TACCG 55

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 55 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION: 1..55  
(D) OTHER INFORMATION: /product= "synthetic  
oligonucleotide"  
/standard\_name= "SM  
80"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

AATTCGGTAC CTATCAGGCC TTCATCTTCT CTTCCATCGC CTTTCATCTTC TCCTC 55

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME/KEY: Protein  
(B) LOCATION: 1..14  
(D) OTHER INFORMATION: /label= name  
/note= "base gene  
[(SSP5)2]"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala  
1 5 10

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid

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(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..21
(D) OTHER INFORMATION: /product=
                        "synthetic
                        oligonucleotide"
                        /standard_name= "SM
                        84"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GATGGAGGAG AAGATGAAGG C 21

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..21
(D) OTHER INFORMATION: /product= "synthetic
                        oligonucleotide"
                        /standard_name= "SM
                        85"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

ATCGCCTTCA TCTTCTCCTC C 21

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..21
(D) OTHER INFORMATION: /product= "synthetic
                        oligonucleotide"
                        /standard_name= "SM
                        82"

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GATGGAGGAG AAGCTGAAGG C

21

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /product= "synthetic  
oligonucleotide"  
/standard\_name= "SM  
83"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

ATCGCCTTCA GCTTCTCCTC C

21

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Met Glu Glu Lys Leu Lys Ala  
1 5

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Met Glu Glu Lys Met Lys Ala  
1 5

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 160 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
  - (B) STRAIN: E. coli
  - (G) CELL TYPE: DH5 alpha
- (vii) IMMEDIATE SOURCE:
  - (B) CLONE: C15
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 2..151
  - (D) OTHER INFORMATION: /function= "synthetic storage protein"  
/product= "protein"  
/gene= "ssp"  
/standard\_name= "5.7.7.7.7.5"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

```
C ATG GAG GAG AAG ATG AAG GCG ATG GAG GAG AAG CTG AAG GCG ATG      46
Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Leu Lys Ala Met
  1              5              10              15

GAG GAG AAG CTG AAG GCG ATG GAG GAG AAG CTG AAG GCG ATG GAG GAG    94
Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu
      20              25              30

AAG CTG AAG GCG ATG GAG GAG AAG CTG AAG GCG ATG GAA GAG AAG ATG 142
Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Met
      35              40              45

AAG GCG TGATAGGTAC CG      160
Lys Ala
      50
```

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 49 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

```
Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu
  1              5              10              15
```

Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys  
 20 25 30

Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Met Lys  
 35 40 45

Ala

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (B) STRAIN: E. coli
- (G) CELL TYPE: DH5 alpha

(vii) IMMEDIATE SOURCE:

- (B) CLONE: C20

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..151
- (D) OTHER INFORMATION: /function= "synthetic storage protein"  
 /product= "protein"  
 /gene= "ssp"  
 /standard\_name= "5.7.7.7.7.5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

C ATG GAG GAG AAG ATG AAG GCG ATG GAG GAG AAG CTG AAG GCG ATG	46
Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Leu Lys Ala Met	
1 5 10 15	
GAG GAG AAG CTG AAG GCG ATG GAG GAG AAG CTG AAG GCG ATG GAG GAG	94
Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu	
20 25 30	
AAG CTG AAG GCG ATG GAG GAG AAG CTG AAG GCG ATG GAA GAG AAG ATG	142
Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Met	
35 40 45	
AAG GCG TGATAGGTAC CG	160
Lys Ala	
50	

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 49 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

```
Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu
 1             5             10             15
Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys
      20             25             30
Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Met Lys
      35             40             45
Ala
```

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 139 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
  - (B) STRAIN: E. coli
  - (G) CELL TYPE: DH5 alpha
- (vii) IMMEDIATE SOURCE:
  - (B) CLONE: C30
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 2..130
  - (D) OTHER INFORMATION: /function= "synthetic  
storage protein"  
/product= "protein"  
/gene= "ssp"  
/standard\_name=  
"5.7.7.7.5"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

```
C ATG GAG GAG AAG ATG AAG GCG ATG GAG GAG AAG CTG AAG GCG ATG      46
Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Leu Lys Ala Met
 1             5             10             15
GAG GAG AAG CTG AAG GCG ATG GAG GAG AAG CTG AAG GCG ATG GAG GAG      94
Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu
      20             25             30
```



AAG CTG AAG GCG ATG GAA GAG AAG ATG AAG GCG TGATAGGTAC CG  
 Lys Leu Lys Ala Met Glu Glu Lys Met Lys Ala  
 35 40

139

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 42 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu  
 1 5 10 15  
 Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys  
 20 25 30  
 Leu Lys Ala Met Glu Glu Lys Met Lys Ala  
 35 40

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 97 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:
  - (B) STRAIN: E. coli
  - (G) CELL TYPE: DH5 alpha

- (vii) IMMEDIATE SOURCE:
  - (B) CLONE: D16

- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 2..88
  - (D) OTHER INFORMATION: /function= "synthetic  
 storage protein"  
 /product= "protein"  
 /gene= "ssp"  
 /standard\_name=  
 "5.5.5.5"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

C ATG GAG GAG AAG ATG AAG GCG ATG GAG GAG AAG ATG AAG GCG ATG 46  
 Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala Met  
 1 5 10 15



GAG GAG AAG ATG AAG GCG ATG GAG GAG AAG ATG AAG GCG ATG GAA GAG 94  
 Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala Met Glu Glu  
 20 25 30

AAG ATG AAG GCG TGATAGGTAC CG 118  
 Lys Met Lys Ala  
 35

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala Met Glu  
 1 5 10 15  
 Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys  
 20 25 30  
 Met Lys Ala  
 35

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 97 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 

- (B) STRAIN: E. coli
- (G) CELL TYPE: DH5 alpha

(vii) IMMEDIATE SOURCE:
 

- (B) CLONE: D33

(ix) FEATURE:
 

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..88
- (D) OTHER INFORMATION: /function= "synthetic storage protein"  
 /product= "protein"  
 /gene= "ssp"  
 /standard\_name= "5.5.5.5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

C ATG GAG GAG AAG ATG AAG GCG ATG GAG GAG AAG ATG AAG GCG ATG 46  
Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala Met  
1 5 10 15  
GAG GAG AAG ATG AAG GCG ATG GAA GAG AAG ATG AAG GCG TGATAGGTAC 95  
Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala  
20 25  
CG 97

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala Met Glu  
1 5 10 15  
Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala  
20 25

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature  
(B) LOCATION: 1..21  
(D) OTHER INFORMATION: /product= "synthetic  
oligonucleotide"  
/standard\_name= "SM  
86"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GATGGAGGAG AAGCTGAAGA A 21

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

```

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
  (A) NAME/KEY: misc_feature
  (B) LOCATION: 1..21
  (D) OTHER INFORMATION: /product= "synthetic
                        oligonucleotide"
                        /standard_name= "SM
                        87"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

ATCTTCTTCA GCTTCTCCTC C
21

(2) INFORMATION FOR SEQ ID NO:43:

  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 21 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

  (ii) MOLECULE TYPE: DNA (genomic)

  (ix) FEATURE:
    (A) NAME/KEY: misc_feature
    (B) LOCATION: 1..21
    (D) OTHER INFORMATION: /product= "synthetic
                        oligonucleotide"
                        /standard_name= "SM
                        88"

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

GATGGAGGAG AAGCTGAAGT G
21

(2) INFORMATION FOR SEQ ID NO:44:

  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 21 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

  (ii) MOLECULE TYPE: DNA (genomic)

  (ix) FEATURE:
    (A) NAME/KEY: misc_feature
    (B) LOCATION: 1..21
    (D) OTHER INFORMATION: /product= "synthetic
                        oligonucleotide"
                        /standard_name= "SM
                        89"

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

ATCCAATTCA GCTTCTCCTC C
21

```

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION: 1..21
  - (D) OTHER INFORMATION: /product= "synthetic  
oligonucleotide"  
/standard\_name= "SM  
90"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

GATGGAGGAG AAGATGAAGA A

21

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION: 1..21
  - (D) OTHER INFORMATION: /product= "synthetic  
oligonucleotide"  
/standard\_name= "SM  
91"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

ATCTTCTTCA TCTTCTCCTC C

21

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION: 1..21

(D) OTHER INFORMATION: /product= "synthetic  
oligonucleotide"  
/standard\_name= "SM  
92"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GATGGAGGAG AAGATGAAGT G

21

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION: 1..21  
(D) OTHER INFORMATION: /product= "synthetic  
oligonucleotide"  
/standard\_name= "SM  
93"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

ATCCACTTCA TCTTCTCCTC C

21

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Met Glu Glu Lys Leu Lys Lys

1 5

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Met Glu Glu Lys Leu Lys Trp  
1 5

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 7 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Met Glu Glu Lys Met Lys Lys  
1 5

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 7 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Met Glu Glu Lys Met Lys Trp  
1 5

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 160 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
(B) STRAIN: E. coli  
(G) CELL TYPE: DH5 alpha

(vii) IMMEDIATE SOURCE:  
(B) CLONE: 82-4

(ix) FEATURE:  
(A) NAME/KEY: CDS  
(B) LOCATION: 2..151  
(D) OTHER INFORMATION: /function= "synthetic  
storage protein  
/product= "protein"



/gene= "ssp"  
 /standard\_name=  
 "7.7.7.7.7.5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

```

C ATG GAG GAG AAG CTG AAG GCG ATG GAG GAG AAG CTG AAG GCG ATG 46
  Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met
    1           5           10          15

GAG GAG AAG CTG AAG GCG ATG GAG GAG AAG CTG AAG GCG ATG GAG GAG 94
  Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu
    20           25          30

AAG CTG AAG GCG ATG GAG GAG AAG CTG AAG GCG ATG GAA GAG AAG ATG 142
  Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Met
    35           40          45

AAG GCG TGATAGGTAC CG 160
  Lys Ala
    50
  
```

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 49 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

```

Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu
  1           5           10          15

Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys
    20           25          30

Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Met Lys
    35           40          45

Ala
  
```

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 97 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:
  - (B) STRAIN: E. coli
  - (G) CELL TYPE: DH5 alpha

(vii) IMMEDIATE SOURCE:  
(B) CLONE: 84-H3

(ix) FEATURE:  
(A) NAME/KEY: CDS  
(B) LOCATION: 2..88  
(D) OTHER INFORMATION: /function= "synthetic  
storage protein  
/product= "protein"  
/gene= "ssp"  
/standard\_name=  
"5.5.5.5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

```
C ATG GAG GAG AAG ATG AAG GCG ATG GAG GAG AAG ATG AAG GCG ATG 46
  Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala Met
    1             5             10             15

GAG GAG AAG ATG AAG GCG ATG GAA GAG AAG ATG AAG GCG TGATAGGTAC 95
  Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala
    20             25

CG 97
```

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

```
Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala Met Glu
  1             5             10             15

Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala
    20             25
```

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 97 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
(B) STRAIN: E. coli  
(G) CELL TYPE: DH5 alpha

(vii) IMMEDIATE SOURCE:  
(B) CLONE: 86-H23

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..88
- (D) OTHER INFORMATION: /function= "synthetic  
storage protein  
/product= "protein"  
/gene= "ssp"  
/standard\_name=  
"5.8.8.5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

```
C ATG GAG GAG AAG ATG AAG GCG ATG GAG GAG AAG CTG AAG AAG ATG 46
  Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Leu Lys Lys Met
    1             5             10             15

GAG GAG AAG CTG AAG AAG ATG GAA GAG AAG ATG AAG GCG TGATAGGTAC 95
  Glu Glu Lys Leu Lys Lys Met Glu Glu Lys Met Lys Ala
    20             25

CG 97
```

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 28 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

```
Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Leu Lys Lys Met Glu
  1             5             10             15

Glu Lys Leu Lys Lys Met Glu Glu Lys Met Lys Ala
    20             25
```

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 112 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
  - (B) STRAIN: E. coli
  - (G) CELL TYPE: DH5 alpha
- (vii) IMMEDIATE SOURCE:
  - (B) CLONE: 88-2

(ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 2..103  
(D) OTHER INFORMATION: /function= "synthetic  
storage protein  
/product= "protein"  
/gene= "ssp"  
/standard\_name=  
"5.9.9.9.5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

C ATG GAG GAG AAG ATG AAG GCG AAG AAG CTG AAG TGG ATG GAG GAG 46  
Met Glu Glu Lys Met Lys Ala Lys Lys Leu Lys Trp Met Glu Glu  
1 5 10 15  
AAG CTG AAG TGG ATG GAG GAG AAG CTG AAG TGG ATG GAA GAG AAG ATG 94  
Lys Leu Lys Trp Met Glu Glu Lys Leu Lys Trp Met Glu Glu Lys Met  
20 25 30  
AAG GCG TGATAGGTAC CG 112  
Lys Ala

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Met Glu Glu Lys Met Lys Ala Lys Lys Leu Lys Trp Met Glu Glu Lys  
1 5 10 15  
Leu Lys Trp Met Glu Glu Lys Leu Lys Trp Met Glu Glu Lys Met Lys  
20 25 30  
Ala

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 118 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(B) STRAIN: E. coli  
(G) CELL TYPE: DH5 alpha

(vii) IMMEDIATE SOURCE:

(B) CLONE: 90-H8

(ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 2..109  
(D) OTHER INFORMATION: /function= "synthetic  
storage protein  
/product= "protein"  
/gene= "ssp"  
/standard\_name=  
"5.10.10.10.5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

```
C ATG GAG GAG AAG ATG AAG GCG ATG GAG GAG AAG ATG AAG AAG ATG 46
  Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Lys Met
    1             5             10             15

GAG GAG AAG ATG AAG AAG ATG GAG GAG AAG ATG AAG AAG ATG GAA GAG 94
  Glu Glu Lys Met Lys Lys Met Glu Glu Lys Met Lys Lys Met Glu Glu
    20             25             30

AAG ATG AAG GCG TGATAGGTAC CG 118
  Lys Met Lys Ala
    35
```

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

```
Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Lys Met Glu
  1             5             10             15

Glu Lys Met Lys Lys Met Glu Glu Lys Met Lys Lys Met Glu Glu Lys
    20             25             30

Met Lys Ala
    35
```

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 97 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(B) STRAIN: E. coli  
(G) CELL TYPE: DH5 alpha

(vii) IMMEDIATE SOURCE:  
(B) CLONE: 92-2

(ix) FEATURE:  
(A) NAME/KEY: CDS  
(B) LOCATION: 2..88  
(D) OTHER INFORMATION: /function= "synthetic  
storage protein  
/product= "protein"  
/gene= "ssp"  
/standard\_name=  
"5.11.11.5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

```
C ATG GAG GAG AAG ATG AAG GCG ATG GAG GAG AAG ATG AAG TGG ATG      46
  Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Trp Met
    1              5              10              15

GAG GAG AAG ATG AAG TGG ATG GAA GAG AAG ATG AAG GCG TGATAGGTAC      95
  Glu Glu Lys Met Lys Trp Met Glu Glu Lys Met Lys Ala
                20              25

CG                                                                    97
```

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

```
Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Trp Met Glu
  1              5              10              15

Glu Lys Met Lys Trp Met Glu Glu Lys Met Lys Ala
    20              25
```

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 84 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION: 1..84  
(D) OTHER INFORMATION: /product= "synthetic  
oligonucleotide"

/standard\_name= "SM  
96"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

GATGGAGGAA AAGATGAAGG CGATGGAGGA GAAAATGAAA GCTATGGAGG AAAAGATGAA 60  
AGCGATGGAG GAGAAAATGA AGGC 84

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..84
- (D) OTHER INFORMATION: /product= "synthetic  
oligonucleotide"  
/standard\_name= "SM  
97"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

ATCGCCTTCA TTTTCTCCTC CATCGCTTTC ATCTTTTCTC CCATAGCTTT CATTTTCTCC 60  
TCCATCGCCT TCATCTTTTC CTCC 84

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..28
- (D) OTHER INFORMATION: /label= name  
/note= "(SSP 5)4"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala Met Glu  
1 5 10 15  
Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala  
20 25

(2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 84 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION: 1..84
  - (D) OTHER INFORMATION: /product= "synthetic  
oligonucleotide"  
/standard\_name= "SM  
98"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

GATGGAGGAA AAGCTGAAAG CGATGGAGGA GAAACTCAAG GCTATGGAAG AAAAGCTTAA 60  
AGCGATGGAG GAGAAACTGA AGGC 84

(2) INFORMATION FOR SEQ ID NO:69:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 84 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION: 1..84
  - (D) OTHER INFORMATION: /product= "synthetic  
oligonucleotide"  
/standard\_name= "SM  
99"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

ATCGCCTTCA GTTCTCCTC CTACGCTTTA AGCTTTTCTT CCATAGCCTT GAGTTTCTCC 60  
TCCATCGCTT TCAGCTTTTC CTCC 84

(2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 28 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: protein



(ix) FEATURE:  
 (A) NAME/KEY: Protein  
 (B) LOCATION: 1..28  
 (D) OTHER INFORMATION: /label= name  
                               /note= "(SSP 7)4"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

```
Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu
1          5          10          15
Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala
          20          25
```

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 84 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 1..84  
 (D) OTHER INFORMATION: /product= "synthetic  
                               oligonucleotide"  
                               /standard\_name= "SM  
                               100"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

```
GATGGAGGAA AAGCTTAAGA AGATGGAAGA AAAGCTGAAA TGGATGGAGG AGAAACTCAA 60
AAAGATGGAG GAAAAGCTTA AATG                                     84
```

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 84 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 1..84  
 (D) OTHER INFORMATION: /product= "synthetic  
                               oligonucleotide"  
                               /standard\_name= "SM  
                               101"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

ATCCATTTAA GCTTTTCCTC CTACTTTTGT AGTTTCTCCT CCATCCATTT CAGCTTTTCT 60  
TCCATCTTCT TAAGCTTTTC CTCC 84

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Met Glu Glu Lys Leu Lys Lys Met Glu Glu Lys Leu Lys Trp Met Glu  
1 5 10 15  
Glu Lys Leu Lys Lys Met Glu Glu Lys Leu Lys Trp  
20 25

(2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 243 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
(B) STRAIN: E. coli  
(G) CELL TYPE: DH5 alpha

(vii) IMMEDIATE SOURCE:  
(B) CLONE: 2-9

(ix) FEATURE:  
(A) NAME/KEY: CDS  
(B) LOCATION: 2..235  
(D) OTHER INFORMATION: /function= "synthetic  
storage protein  
/product= "protein"  
/gene= "ssp"  
/standard\_name=  
"7.7.7.7.7.7.8.9.8.9.5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

C ATG GAG GAG AAG CTG AAG GCG ATG GAG GAG AAG CTG AAG GCG ATG 46  
Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met  
1 5 10 15

GAG GAG AAG CTG AAG GCG ATG GAG GAG AAG CTG AAG GCG ATG GAG GAG 94  
 Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu  
                   20                                  25                                  30

AAG CTG AAG GCG ATG GAG GAG AAG CTG AAG GCG ATG GAG GAA AAG CTT 142  
 Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu  
                   35                                  40                                  45

AAG AAG ATG GAA GAA AAG CTG AAA TGG ATG GAG GAG AAA CTC AAA AAG 190  
 Lys Lys Met Glu Glu Lys Leu Lys Trp Met Glu Glu Lys Leu Lys Lys  
                   50                                  55                                  60

ATG GAG GAA AAG CTT AAA TGG ATG GAA GAG AAG ATG AAG GCG TGATAGGTAC 242  
 Met Glu Glu Lys Leu Lys Trp Met Glu Glu Lys Met Lys Ala  
           65                                  70                                  75

C

243

(2) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 77 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu  
   1                                  5                                  10                                  15

Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys  
                   20                                  25                                  30

Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys  
                   35                                  40                                  45

Lys Met Glu Glu Lys Leu Lys Trp Met Glu Glu Lys Leu Lys Lys Met  
           50                                  55                                  60

Glu Glu Lys Leu Lys Trp Met Glu Glu Lys Met Lys Ala  
   65                                  70                                  75

(2) INFORMATION FOR SEQ ID NO:76:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 175 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:
  - (B) STRAIN: E. coli
  - (G) CELL TYPE: DH5 alpha

(vii) IMMEDIATE SOURCE:

(B) CLONE: 5-1

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 2..172

(D) OTHER INFORMATION: /function= "synthetic  
storage protein  
/product= "protein"  
/gene= "ssp"  
/standard\_name=  
"5.5.5.7.7.7.5"

(xi) . SEQUENCE DESCRIPTION: . SEQ ID NO:76:

```
C ATG GAG GAG AAG ATG AAG GCG ATG GAG GAG AAG ATG AAG GCG ATG      46
Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala Met
   1             5             10             15

GAG GAG AAG ATG AAG GCG ATG GAG GAA AAG CTG AAA GCG ATG GAG GAG      94
Glu Glu Lys Met Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu
                20             25             30

AAA CTC AAG GCT ATG GAA GAA AAG CTT AAA GCG ATG GAG GAG AAA CTG      142
Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu
                35             40             45

AAG GCC ATG GAA GAG AAG ATG AAG GCG TGATAG                          175
Lys Ala Met Glu Glu Lys Met Lys Ala
   50             55
```

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 56 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) . SEQUENCE DESCRIPTION: SEQ ID NO:77:

```
Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala Met Glu
   1             5             10             15

Glu Lys Met Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys
                20             25             30

Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys
                35             40             45

Ala Met Glu Glu Lys Met Lys Ala
   50             55
```

(2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 187 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
  - (B) STRAIN: E. coli
  - (G) CELL TYPE: DH5 alpha
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 3..173
  - (D) OTHER INFORMATION: /function= "synthetic  
storage protein  
/product= "protein"  
/gene= "ssp"  
/standard\_name=  
"SSP-3-5"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

```
CC ATG GAG GAG AAG CTG AAG GCG ATG GAG GAG AAG CTG AAG GCG ATG      47
   Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met
     1             5             10             15

GAG GAG AAG CTG AAG GCG ATG GAG GAG AAG CTG AAG GCG ATG GAG GAG      95
   Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu
             20             25             30

AAG CTG AAG GCG ATG GAG GAG AAG CTG AAG GCG ATG GAG GAA AAG ATG     143
   Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Met
             35             40             45

AAG GCG ATG GAA GAG AAG ATG AAG GCG TGATAGGTAC CGAATTC             187
   Lys Ala Met Glu Glu Lys Met Lys Ala
     50             55
```

(2) INFORMATION FOR SEQ ID NO:79:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 56 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

```
Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu
   1             5             10             15

Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys
   20             25             30
```

Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Met Lys  
                   35                                  40                                  45

Ala Met Glu Glu Lys Met Lys Ala  
           50                                  55

(2) INFORMATION FOR SEQ ID NO:80:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 61 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION: 1..61
  - (D) OTHER INFORMATION: /product= "synthetic  
                                   oligonucleotide"  
                                   /standard\_name= "SM  
                                   107"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

CATGGAGGAG AAGATGAAAA AGCTCGAAGA GAAGATGAAG GTCATGAAGT GATAGGTACC 60  
 G 61

(2) INFORMATION FOR SEQ ID NO:81:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 61 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION: 1..61
  - (D) OTHER INFORMATION: /product= "synthetic  
                                   ligonucleotide"  
                                   /standard\_name= "SM  
                                   106"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

AATTCGGTAC CTATCACTTC ATGACCTTCA TCTTCTCTTC GAGCTTTTTC ATCTTCTCCT 60  
 C 61

(2) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: protein
- (ix) FEATURE:
  - (A) NAME/KEY: Protein
  - (B) LOCATION: 1..16
  - (D) OTHER INFORMATION: /label= name  
/note= "pSK34 base  
gene"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Met Glu Glu Lys Met Lys Lys Leu Glu Glu Lys Met Lys Val Met Lys  
1                      5                      10                      15

(2) INFORMATION FOR SEQ ID NO:83:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 63 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION: 1..63
  - (D) OTHER INFORMATION: /product= "synthetic  
oligonucleotide"  
/standard\_name= "SM  
110"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

GCTGGAAGAA AAGATGAAGG CTATGGAGGA CAAGATGAAA TGGCTTGAGG AAAAGATGAA 60  
GAA 63

(2) INFORMATION FOR SEQ ID NO:84:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 63 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 1..63  
 (D) OTHER INFORMATION: /product= "synthetic  
 oligonucleotide"  
 /standard\_name= "SM  
 111"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

AGCTTCTTCA TCTTTTCCTC AAGCCATTTC ATCTTGTCCT CCATAGCCTT CATCTTTTCT 60  
 TCC 63

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 37 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

Met Glu Glu Lys Met Lys Lys Leu Glu Glu Lys Met Lys Ala Met Glu  
 1 5 10 15  
 Asp Lys Met Lys Trp Leu Glu Glu Lys Met Lys Lys Leu Glu Glu Lys  
 20 25 30  
 Met Lys Val Met Lys  
 35

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 37 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Met Glu Glu Lys Met Lys Lys Leu Glu Glu Lys Met Lys Ala Met Glu  
 1 5 10 15  
 Asp Lys Met Lys Trp Leu Glu Glu Lys Met Lys Lys Leu Glu Glu Lys  
 20 25 30  
 Met Lys Val Met Lys  
 35



(2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 62 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION: 1..62
  - (D) OTHER INFORMATION: /product= "synthetic  
oligonucleotide"  
/standard\_name= "SM  
112"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

GCTCGAAGAA AGATGAAGGC AATGGAAGAC AAAATGAAGT GGCTTGAGGA GAAAATGAAG 60  
AA 62

(2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 62 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION: 1..62
  - (D) OTHER INFORMATION: /product= "synthetic  
oligonucleotide"  
/standard\_name= "SM  
113"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

AGCTTCTTCA TTTTCTCCTC AAGCCACTTC ATTTTGTCTT CCATTGCCTT CATCTTTCTT 60  
CG 62

(2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

Met Glu Glu Lys Met Lys Lys Leu Lys Glu Glu Met Ala Lys Met Lys  
1 5 10 15  
Asp Glu Met Trp Lys Leu Lys Glu Glu Met Lys Lys Leu Glu Glu Lys  
20 25 30  
Met Lys Val Met Lys  
35

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..63
- (D) OTHER INFORMATION: /product= "synthetic  
oligonucleotide"  
/standard\_name= "SM  
114"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

GCTCAAGGAG GAAATGGCTA AGATGAAAGA CGAAATCTGG AAAGTGAAG AGGAAATGAA 60  
GAA 63

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..63
- (D) OTHER INFORMATION: /product= "synthetic  
oligonucleotide"  
/standard\_name= "SM  
115"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

AGCTTCTTCA TTTCCTCTTT CAGTTTCCAC ATTTCGTCTT TCATCTTAGC CATTTCTTCC 60  
TTG 63

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

Met Glu Glu Lys Met Lys Lys Leu Lys Glu Glu Met Ala Lys Met Lys  
1 5 10 15  
Asp Glu Met Trp Lys Leu Lys Glu Glu Met Lys Lys Leu Glu Glu Lys  
20 25 30  
Met Lys Val Met Glu Glu Lys Met Lys Lys Leu Glu Glu Lys Met Lys  
35 40 45  
Ala Met Glu Asp Lys Met Lys Trp Leu Glu Glu Lys Met Lys Lys Leu  
50 55 60  
Glu Glu Lys Met Lys Val Met Glu Glu Lys Met Lys Lys Leu Glu Glu  
65 70 75 80  
Lys Met Lys Ala Met Glu Asp Lys Met Lys Trp Leu Glu Glu Lys Met  
85 90 95  
Lys Lys Leu Glu Glu Lys Met Lys Val Met Lys  
100 105

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 839 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

GGATCCCCCG GGCTGCAGGA ATTCTACGTA CCATATAGTA AGACTTTGTA TATAAGACGT 60  
CACCTCTTAC GTGCATGGTT ATATGTGACA TGTGCAGTGA CGTTGTACCA TATAGTAAGA 120  
CTTTGTATAT AAGACGTCAC CTCTTACGTG CATGGTTATA TGTGACATGT GCAGTGACGT 180  
TAACCGCACC CTCCTTCCCG TCGTTTCCCA TCTCTTCCTC CTTTAGAGCT ACCACTATAT 240  
AAATCAGGGC TCATTTTCTC GCTCCTCACA GGCTCATCAG CACCCCGGCA GTGCCACCCC 300  
GACTCCCTGC ACCTGCCATG GGTACGCTAG CCCGGGAGAT CTGACAAAGC AGCATTAGTC 360  
CGTTGATCGG TGGAAGACCA CTCGTCAGTG TTGAGTTGAA TGTTTGATCA ATAAAATACG 420

GCAATGCTGT AAGGGTTGTT TTTTATGCCA TTGATAATAC ACTGTACTGT TCAGTTGTTG 480  
 AACTCTATTT CTTAGCCATG CCAGTGCTTT TCTTATTTTG AATAACATTA CAGCAAAAAG 540  
 TTGAAAGACA AAAAAANNNN NCCCCGAACA GAGTGCTTTG GGTCCCAAGC TTCTTTAGAC 600  
 TGTGTTGCGC GTTCCCCCTA AATTTCTCCC CTATATCTCA CTCACTTGTC ACATCAGCGT 660  
 TCTCTTTCCC CTATATCTCC ACGCTCTACA GCAGTTCCAC CTATATCAAA CCTCTATACC 720  
 CCACCACAAC AATATTATAT ACTTTCATCT TCACCTAACT CATGTACCTT CCAATTTTTT 780  
 TCTACTAATA ATTATTTACG TGCACAGAAA CTTAGGCAAG GGAGAGAGAG AGCGGTACC 839

(2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 43 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

CTAGAAGCCT CGGCAACGTC AGCAACGGCG GAAGAATCCG GTG 43

(2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 43 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

CATGCACCGG ATTCTTCCGC CGTTGCTGAC GTTGCCGAGG CTT 43

(2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 55 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

GATCCCATGG CGCCCCTTAA GTCCACCGCC AGCCTCCCCG TCGCCCGCCG CTCCT 55

(2) INFORMATION FOR SEQ ID NO:97:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 55 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

CTAGAGGAGC GCGGGGCGAC GGGGAGGCTG GCGGTGGACT TAAGGGGCGC CATGG 55

(2) INFORMATION FOR SEQ ID NO:98:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 59 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

CATGGCGCCC ACCGTGATGA TGGCCTCGTC GGCCACCGCC GTCGCTCCGT TCCAGGGGC 59

(2) INFORMATION FOR SEQ ID NO:99:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 59 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

TTAAGCCCCT GGAACGGAGC GACGGCGGTG GCCGACGAGG CCATCATCAC GGTGGGCGC 59

(2) INFORMATION FOR SEQ ID NO:100:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

GCGCCACCG TGATGA

16

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

CACCGGATTC TTCCGC

16

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

GTAAGATTGG TAAAGTCCAG CAAGAAAATG AGATAAAAGA GAAGCCTGAA ATGACGAAAA 60  
AATCAGGTGT TTTGATTCTT GGTGCTGGAC GTGTGTNTCG CCCAGCTGCT GATTCCTAG 120  
CTTCAGTTAG AACCATTTTCG TCACAGCAAT GGTACAAAAC ATATTTTCGGA GCAGACTCTG 180  
AAGAGAAAAC AGATGTTTCAT GTGATTGTCG CGTCTCTGTA TCTTAAGGAT GCCAAAGAGA 240  
CGGTTGAAGG TATTTTCAGAT GTAGAAGCAG TTCGGCTAGA TGTATCTGAT AGTGAAAGTC 300  
TCCTTAAGTA TGTTTCTCAG GTTGATGTTG TCCTAAGTTT ATTACCTGCA AGTTGTCATG 360  
CTTGTTGTAG CA 372

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

GGAAGCACAC TCGACTCTT TTGGAATTCG GGGACATCAA GAATGGACAA ACAACAACCG 60  
CTATGGCCAA GACTGTTGGG ATCCCTGCAG CCATTGGAGC TCTGCTGTTA ATTGAAGACA 120  
AGATCAAGAC AAGAGGAGTC TTAAGGCCTC TCGAAGCAGA GGTGTATTG CCAGCTTTGG 180

ATATATTGCA AGCATATGGT ATAAAGCTGA TGGAGAAGGC AGAATGATCA AAGAACTCTG 240  
TATATTGTTT CTNTCTATAA CTTGGAGTTG GAGACAAAGC TGAAGGAGNC AGNGCCATTA 300  
GACCAGCAAA AAAAGGAGGA GGA 323

(2) INFORMATION FOR SEQ ID NO:104:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 123 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

Lys Ile Gly Lys Val Gln Gln Glu Asn Glu Ile Lys Glu Lys Pro Glu  
1 5 10 15  
Met Thr Lys Lys Ser Gly Val Leu Ile Leu Gly Ala Gly Arg Val Xaa  
20 25 30  
Arg Pro Ala Ala Asp Phe Leu Ala Ser Val Arg Thr Ile Ser Ser Gln  
35 40 45  
Gln Trp Tyr Lys Thr Tyr Phe Gly Ala Asp Ser Glu Glu Lys Thr Asp  
50 55 60  
Val His Val Ile Val Ala Ser Leu Tyr Leu Lys Asp Ala Lys Glu Thr  
65 70 75 80  
Val Glu Gly Ile Ser Asp Val Glu Ala Val Arg Leu Asp Val Ser Asp  
85 90 95  
Ser Glu Ser Leu Leu Lys Tyr Val Ser Gln Val Asp Val Val Leu Ser  
100 105 110  
Leu Leu Pro Ala Ser Cys His Ala Cys Cys Ser  
115 120

(2) INFORMATION FOR SEQ ID NO:105:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 74 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

Lys His Thr Ala Thr Leu Leu Glu Phe Gly Asp Ile Lys Asn Gly Gln  
1 5 10 15

Thr Thr Thr Ala Met Ala Lys Thr Val Gly Ile Pro Ala Ala Ile Gly  
 20 25 30  
 Ala Leu Leu Leu Ile Glu Asp Lys Ile Lys Thr Arg Gly Val Leu Arg  
 35 40 45  
 Pro Leu Glu Ala Glu Val Tyr Leu Pro Ala Leu Asp Ile Leu Gln Ala  
 50 55 60  
 Tyr Gly Ile Lys Leu Met Glu Lys Ala Glu  
 65 70

(2) INFORMATION FOR SEQ ID NO:106:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

ATTCCCCATG GTTTCGCCGA CGAAT

25

(2) INFORMATION FOR SEQ ID NO:107:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

CTCTCGGTAC CTAGTACCTA CTGATCAAC

29

(2) INFORMATION FOR SEQ ID NO:108:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

AGAGAAGCCT GAAATGACGA AAAA

24



(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

GTCTTGGCCA TAGCGGTTGT TGTT

24

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8160 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

TCTAGATGCA CATTCAACTC GAGGTTGTTG CATGATGTTT CATTTACCAA AAAAATCATA	60
GTCAAATTAT GTAAGCAAAT GATATTACAG AAAAGTTTCTA CTAGAGAGTT TCAGATTTAC	120
ACATGCACAA CGTTAAAAAA AATAGCAGAA AAAAGAAAGA AGAAAAGTTC TTTATTTGTG	180
AGAAAAATGT ATGAAAAAAA AAGAGATGGG TGTA AAAAGC AAAAGGATAG GACCACTGTT	240
ACTTTGTAGC CTCGTTGAGG AATCTCTTCT CGCATCTCGA CTTTGTGCC ATTGCAAAGT	300
CAATGCCCAG AACTTGTTCC CAGGCCATCT CCAATTAAC TACGTCTATTT AATTAACTT	360
TTAAAAGAAA ACCTAATAAA TTAAACAAAA GAAAGCCGT CAACGAAATC TAAGCTTGCA	420
GCGATATCGA TGAAGTATA CAAAACAAT GTTCAAGTTT CACTTTCAAA TTGTTTTTTC	480
TTGAAATAGT TTATTGGGTA AGGCCCATAG ATATTTTATA AGAAGAACAC TTGTCGAGGT	540
TGAATCGTAT GTCTGCCCAC CGCGGCCCAT GCATCCTCTG TTGGTAGCAT AATCGTTTTA	600
GGCCATACTA TTGTTGTTAC AACTGATTT TGAAGTCACC TTTGTGCACT CCTTAATTCC	660
TAAATTGAAG AAGCTTGTTT TCATTCTTCT TTGGGTTACA AATGCCAAGG CAAAAGGAAC	720
TTGGGCCAAA TTAAGACAAC, AACTCAAGCC CACTCTCTGC AAATAATACT TGGGAATTTT	780
TACTAAAACG GTGCGTTTCA TCCAAGAATC TATTAATATC CCTAACTTGA AATCATCATA	840
TACGTAACCC AACATATTAA AGAGTTAATA ATGTTAAAAA AAGTCTCAGA AGAGAGAGAC	900
GTAGAGAACA CGGAAAGTGG TAACTGGTAA GCGTCGTCAT CGAGGATATA GTAGCTACGT	960

GAGCAAACGT	CTTCACTCAT	CTCTGTCTAT	TTCTCTTCGA	ATACACGTAA	TACATTTTCG	1020
ATTGGATTGA	TCCTCCCTCG	GTCCTATCCA	AGTATCCATC	CACGTAAACA	AGAGCTTGTT	1080
CCTTTCTTGT	TTTTTCTTTC	TTTAAATAGT	AAAAATACTT	ATTTTCATTG	TTTCGTTTGA	1140
TTTCATTATT	ATTGTCTATG	GCATTATATA	CTATATATAT	TATTTCTACA	ACATTGGCTG	1200
GCTCACGTTG	TTCTCGTGTA	TACAACAAAC	TTAATTAATG	TCTCTCTATT	GCATTAGATA	1260
GTTTCGGAGC	ATATCCATTA	TGTGAAAGCC	ACATTAAGTT	ATAACTAAAA	GTAGTTTTTCG	1320
AAAGAGCTTA	ATTAAGTTAT	GTTCTGTTTC	AAATAAAAAT	GAACACGAGG	GATTTTTTTTT	1380
TTTTTTGACA	GATCATTATT	AACAAAAATG	ATTACCTGAA	GAAAGGGGAA	AATAATTATA	1440
GCTGATTACA	GATCATTATT	AACAAAAAGA	ATTCTTGTC	CATCATTTCAT	TATAACAAGA	1500
AATATTATAT	TATATTAATT	TAATCTTTCG	CTAACACGCC	CACAATATAT	TAATCATATA	1560
CGTAATTTAG	CTTATAAAAA	GGACGGAAAG	AGATTATTAC	TGCGCCTAAA	AACTCACTA	1620
ATTCCAAAGA	AAAAAAAAAAG	CTTGTATTTT	TTCTTGACAA	ACCAGCTCAC	AGGCATTGCA	1680
TGATCAAAC	CATCAGGTAC	GTTTTGATTC	CTTCTTCCAT	AATTTTCCCA	TCTTGAGGAA	1740
TGCAAATTTG	GAGAGCGCTT	TAGCTAAATC	ACTGCCTTCA	TTTTTTTCACT	TTGGATTATA	1800
TAATTTGCAT	TCCTCTCTTC	CTCTCTGCTC	TGTTCTGTTT	TGTTCTGTTC	TGATTTGAGT	1860
TTTCAATTAA	TCGCTCGAGC	AAAAGCTATT	TCTCAACTCG	TTAAATTTCT	GTTCCCAGTT	1920
TGTTTCGATTT	TCAACAGTTT	CACATTAAAG	TTTGGGTTTT	TGATGTTTGG	TTGATGAAAC	1980
TCGAAATATG	AAATGTTTGT	GAATCTATTC	CAGGGTGTTT	AAAATAAGGG	TTTGTGTGTT	2040
ATCTGCAGAG	ATTATATGTT	TTTACATGAA	AGATGAATTC	AAATGGCCAT	GAGGAGGAGA	2100
AGAAGTTGGG	GAATGGAGTT	GTGGGGATTC	TAGCTGAAAC	AGTTAACAAA	TGGGAGAGAC	2160
GAACACCATT	GACGCCATCG	CATTGCGCTC	GCCTTTTACA	CGGTGGGAAA	GACAGAACCG	2220
GCATTTCCCG	CATTGTGGTT	CAGCCATCTG	CTAAGCGTAT	CCATCATGAT	GCCTTGTATG	2280
AAGATGTTGG	GTGTGAAATT	TCTGATGATT	TGTCTGATTG	TGGGCTTATA	CTTGGAAATCA	2340
AACAACCTGA	GGTGTGGGAA	TTTGCATTAA	AAAGAGTTCC	TTTTTTTCTT	CTATATATAT	2400
ATCAGTTTAT	GAGATTTGAT	TCTGTTTGCA	GCTAGAAATG	ATTCTTCCAG	AGAGAGCATA	2460
CGCTTTCTTT	TCACATACTC	ATAAGGCACA	GAAAGAGAAC	ATGCCTTTGT	TGGATAAAGT	2520
ATTACACTTT	TCATTTATCC	TTTGTAGTCT	ATCTAAGATA	CTGAGGAATG	TTGACAAAAG	2580
GGGTATCCAA	TTGCAGATTC	TTTCTGAGAG	AGTGACTTTG	TGTGATTATG	AGCTCATTGT	2640
TGGGGATCAT	GGGAAACGAT	TATTGGCGTT	TGGTAAATAT	GCAGGCAGAG	CTGGTCTTGT	2700

TGACTTCTTA	CACGGACTTG	GACAGCGTAA	GCTCATGTTA	TAATTCTGAT	GATCAGGACA	2760
TGTTTCTGTG	CAGAACAAGA	TGAGATGTAA	TTTTCCATGT	TTGATGCAGG	ATATCTAAGT	2820
CTAGGATACT	CAACACCTTT	CCTCTCGCTC	GGTGCATCGT	ATATGTATTC	CTCATTGGCT	2880
GCTGCAAAAG	CCGCTGTAAT	TTCTGTTGGT	GAAGAAATTG	CAAGCCAGGG	ACTGCCATTA	2940
GGAATCTGCC	CTCTTGATT	TGTCTTCACC	GGAACAGGAA	ATGGTATCTT	CTTTAGTTCT	3000
ACTGCGAGTT	CTTTGAATCC	TTCTGCATAT	GTTTCATCTC	ATTAAAAAAT	TTCTCATCCG	3060
CAGTTTCTCT	GGGGGCGCAA	GAAATTTTCA	AGCTTCTTCC	TCACACTTTT	GTTGAACCAA	3120
GCAAACCTCC	TGAACTATTT	GTAAAAGTAA	GTCACGCTTT	GCTTTTTTATT	TGGTTTCAGA	3180
GTTTTGAAGA	TTCTGAAATG	TATATTTCTC	ACAGGACAAA	GGAATTAGTC	AAAATGGGAT	3240
TTCAACAAAG	CGAGTCTATC	AAGTATATGG	TTGTATTATT	ACCAGCCAAG	ACATGGTTGA	3300
ACACAAAGAT	CCATCAAAGT	CATTGACAAA	AGTAACACTT	ACCTTCTTAG	CTCCTTGGCT	3360
GTGACTTTTG	TTCCACTACG	CTAAAGTAGA	ATACCTATTA	ATTCTTCAAG	CTTATGATGT	3420
TTAGGCCGAC	TATTATGCAC	ACCCGGAACA	TTACAATCCA	GTTTTCCACG	AAAAGATATC	3480
GCCATATACG	TCTGTTCTTG	GTAGATCCTG	ATCACTGTTT	TACCTTTAAA	GCTCAAGAGT	3540
TTACATATAA	GCAAATCCTC	TGTCCACTCC	GTGACTGTGA	CCATCTCATT	TTGGTTAGTT	3600
CCAGTGTGTA	ACCCCTATGA	CTTTCTGTGC	AGTAAACTGT	ATGTACTGGG	AGAAGAGGTT	3660
TCCCTGTCTT	CTGAGCACAA	AACAGCTTCA	AGATTTAACA	AAAAAAGGAC	TCCCACTAGT	3720
AGGCATATGT	GATATAACTT	GTGACATCGG	TGGCTCCATT	GAATTTGTTA	ACCGAGCTAC	3780
TTTAATCGAT	TCCCCTTTCT	TCAGGTAATA	TATACTTAGG	AAGAGCTTTC	TTTTGAGTCA	3840
TCTACGTTTA	CTATGATGAA	ACTCGTCGAG	CTAAACACTA	TCTCTAGGTT	TAATCCCTCG	3900
AACAATTCAT	ACTACGATGA	CATGGATGGG	GATGGCGTAC	TATGCATGGC	TGTTGACATT	3960
TTACCCACAG	AATTTGCAAA	AGAGGTATGT	ATGAAGGTTA	CAGTTATAGT	ACTTAAGATT	4020
AAATCTAAAG	TTAAAAACCT	TGTATTGAGT	GGGAGTTCTT	GTGTCCTGAA	AAAGGCATCC	4080
CAGCATTTTG	GAGATATTCT	TTCCGGATTT	GTCGGTAGTT	TGGCTTCAAT	GACTGAAATT	4140
TCAGATCTAC	CAGCACATCT	GAAGAGGGCT	TGCATAAGCT	ATAGGGGAGA	ATTGACATCT	4200
TTGTATGAGT	ATATTCCACG	TATGAGGAAG	TCAAATCCAG	AGTATGTTCT	GCTTCGAGCG	4260
TTACTTCATC	TGAAATATTT	AGGCCTCTTC	TCTAAACTAT	GTTTTCATCT	TTACCCACTT	4320
TAAGTGCAGA	GAGGCACAAG	ATAATATTAT	CGCCAACGGG	GTTTCCAGCC	AGAGAACATT	4380
CAACATATTG	GTTAGTTTTG	ATGAAGAAAG	TATATATAAC	TAGTTTCCGA	ATCATATGAT	4440

TTAAGCTAAT GAATTAAGAA AATATATAGT TCAAGACTTA TGATTCATAT CTCTATCAAC 4500  
 TTTTGGACCA AAGATTGATA CTTTTTCGAC ATCTGTCACA GCATTTTGTG ATGATTTTGA 4560  
 TTGAGACAAA TCATTTGTAG GTATCTCTGA GCGGACACCT ATTTGATAAG TTTCTGATAA 4620  
 ACGAAGCTCT TGATATGATC GAAGCGGCTG GTGGCTCATT TCATTTGGCT AAATGTGAAC 4680  
 TGGGGCAGAG CGCTGATGCT GAATCGTACT CAGAACTTGA AGTAAGTTTC TTTCTGGATA 4740  
 AAACCTAATC ATTCACATGG AACAACTGTC AAGAGTTTTT AATGTCACGT TTAGGTTCAA 4800  
 TGTCCTTTTC ACTAAGTCTC GTAAGTTTTT AAAACAAGTA AACAAACTAC AAGCCAAAAA 4860  
 CATTCTGGCC CCACATTAAC CTATTCCCAC TTGTTAAAGA ACCCATCTTG CATTATCTTG 4920  
 GTAGGTTGGT GCGGATGATA AGAGAGTATT GGATCAAATC ATTGATTCAT TAACTCGGTT 4980  
 AGCTAATCCA AATGAAGATT ATATATCCCC ACATAGAGAA GCAAATAAGA TCTCACTGAA 5040  
 GATTGGTAAA GTCCAGCAAG AAAATGAGAT AAAAGAGAAG CCTGAAATGA CGAAAAAATC 5100  
 AGGCGTTTTG ATTCTTGGTG CTGGACGTGT GTGTCGCCCA GCTGCTGATT TCCTAGCTTC 5160  
 AGTTAGAACC ATTTTCGTCAC AGCAATGGTA CAAAACATAT TTCGGAGCAG ACTCTGAAGA 5220  
 GAAACAGAT GTTCATGTGA TTGTCGCGTC TCTGTATCTT AAGGATGCCA AAGAGGTAGG 5280  
 AGAAGCCTTT GGGCTTCATC TGAGTAATTC AGTGTATACG ATGAACTATC AATCTTTTAA 5340  
 AGTTTTACTG ATGATCAAAT TTTCCGCAGA CGGTTGAAGG TATTTTCAGAT GTAGAAGCAG 5400  
 TTCGGCTAGA TGTATCTGAT AGTGAAAGTC TCCTTAAGTA TGTTTCTCAG GTATTTTCCT 5460  
 AACTTCTCTG TTCTTAGATC ACCTTTACTT CAACTCCAC TGTTCAAATC CATGATCTTA 5520  
 TATTTTTTTT TCATTGCACG CAGGTTGATG TTGTCCTAAG TTTATTACCT GCAAGTTGTC 5580  
 ATGCTGTTGT AGCAAAGACA TGCATTGAGG TAAATTCCTA ACGTTTAATG CGTTTTCCGA 5640  
 GTGAAGTTAT GAAATTTGCA AATGTTATTC GACATAGAGG TTAAACTTCC TCTGCATAAC 5700  
 ACATTCTTTC AGTAGTTTCC GGTTCCTAAA TGTCTCTGTT TCTTCTTCTT GATTCACCTCA 5760  
 GCTGAAGAAG CATCTCGTCA CTGCTAGCTA TGTTGATGAT GAAACGTCCA TGTTACATGA 5820  
 GAAGGCTAAG AGTGCTGGGA TAACGATTCT AGGCGAAATG GGAAGTGGACC CTGGAATCGG 5880  
 TATGATATCT CACAACATAG TATCTCTTAA GATCATTTGT TCACTTGATT TAACTTAAGT 5940  
 GCATTTATCT TCAAAATATT TCCCGGATAA CTGAGAAGGT GATCCTACAA TGAATCTTTC 6000  
 AGATCACATG ATGGCGATGA AAATGATCAA CGATGCTCAT ATCAAAAAAG GGAAAGTGAA 6060  
 GTCTTTTACC TCTTATTGTG GAGGGCTTCC CTCTCCTGCT GCAGCAAATA ATCCATTAGC 6120  
 ATATAAATTT AGGTACGGTA GTCCTTTACG CCATTAACAT ATTTTGTTTT GTTTAACTCA 6180

TTTAGACATC	CTTTCAGAAT	TTCGCTTACT	CAATTACATC	TCGGTATTTT	CAGCTGGAAC	6240
CCTGCTGGAG	CAATTTCGAGC	TGGTCAAAAAC	CCCGCCAAAT	ACAAAAGCAA	CGGCGACATA	6300
ATACATGTTG	ATGGTATGAA	AAACAAAATA	TGTCTACATG	CAGGAGAGGT	TGGAGTAGTT	6360
TAGCTTCACT	ACACATCATT	TTTGTTTAAC	CGAGCAATGT	AAATCGCAGG	GAAGAATCTC	6420
TATGATTCCG	CGGCAAGATT	CCGAGTACCT	AATCTTCCAG	CTTTTGCATT	GGAGTGTCTT	6480
CCAAATCGTG	ACTCCTTGGT	TTACGGGGGAA	CATTATGGCA	TCGAGAGCGA	AGCAACAACG	6540
ATATTTTCGTG	GAACACTCAG	ATATGAAGGC	ATGAATTCCA	TAATCACAAC	TCACGACTCA	6600
CTTCTCCATA	TCTGAAGGCT	TAACACTTGT	TTTCTTTTGG	CTTGTACAGG	GTTTAGTATG	6660
ATAATGGCAA	CACTTTTCGAA	ACTTGGATTG	TTTGACAGTG	AAGCAAATCA	AGTACTCTCC	6720
ACTGGAAAGA	GGATTACGTT	TGGTGCTCTT	TTAAGTAACA	TTCTAAATAA	GGATGCCGAC	6780
AATGAATCAG	AGCCCCTAGC	GGGAGAAGAA	GAGATAAGCA	AGAGAATTAT	CAAGCTTGGA	6840
CATTCCAAGG	AGACTGCAGC	CAAAGCTGCC	AAAACAATTG	TGTAAGCTTC	TCCATGAAGA	6900
TATATAATCT	GAATGTTGCA	GTGTGATTCC	AATTCTTCTA	CGAAACTCCT	AACCCCAATT	6960
CTTTTGTGGT	GTCTTAGATT	CTTGGGGTTC	AACGAAGAGA	GGGAGGTTCC	ATCACTGTGT	7020
AAAAGCGTAT	TTGATGCAAC	TTGTTACCTA	ATGGAAGAGA	AACTAGCTTA	TTCCGGAAAT	7080
GAACAGGTCT	CTGTTTCATG	TGAAAGCATT	AGTTTTCTTC	TCTCACTTGT	ATTTGGTGTT	7140
ACTTACTGAC	ATAAACTTTG	GACAATCTTT	TGCATTATGT	TTTCAGGACA	TGGTGCTTTT	7200
GCATCACGAA	GTAGAAGTGG	AATTCCTTGA	AAGCAAACGT	ATAGAGAAGC	ACACTGCGAC	7260
TCTTTTGGAA	TTCGGGGACA	TCAAGAATGG	GCAAACAACA	ACCGCTATGG	CCAAGACTGT	7320
TGGGATCCCT	GCAGCCATTG	GAGCTCTGGT	CCTTACTAAG	ACTTTGATCA	CCACTTTTTT	7380
CTGTCTATAT	TTCTCTAAAA	TGAAAGTTTT	AAGCGTTTGT	TTTATGATGT	TGTGTGTTGC	7440
AGCTGTTAAT	TGAAGACAAG	ATCAAGACAA	GAGGAGTCTT	AAGGCCTTTC	GAAGCAGAGG	7500
TGTATTTGCC	AGGTAAATTA	GAATTCCGCT	TCAAAGGAT	GTGTGTTGCA	GATAAAGACA	7560
ATGATGTTGA	TTTGTTGTGT	GTTTGGGATA	TGTGGTGTTA	TACATACAGC	TTTGGATATA	7620
TTGCAAGCAT	ATGGTATAAA	GCTGATGGAG	AAGGCAGAAT	GATCAAAGAA	CTCTGTATAT	7680
TGTTTCTCTC	TATAACTTGG	AGTTGGAGAC	AAAGCTGAAG	AAGACAGAGA	CATTAGACCA	7740
GCAAAAAAAG	AAGAAGAAGG	AAGAAGATAA	GCCTCGATCC	TTGGGTGACG	AGTATCTATA	7800
TGTTTATATG	TACTATATGT	TATGTTGTAC	AGAAGAAGTC	GTGTCCACAA	ATATCAATTG	7860
ATGTCAGATG	TCTAGTAAGT	GATCATGTGT	AGCATACAAA	CTGGAGTAAT	TTAAAAAGTG	7920

AATAAACAAA AATAATTACT AAACGTTATT CCAAGTAGCT TTCCAAGACA GTCACTTGCC 7980  
 CTTTTCCAAT TTCCCTTGCA ATTAATAAAA TTGCTCTTCA CGATATGATA TTATACCAAA 8040  
 ATGGTGATAC CTTGGGAATT GTTAATTTGA CTCATTTGAA CAAATCTCAT CTATAAAATC 8100  
 ATCCACCTC TCCACCACAT TTGTTCTCAC TACCAATCAA AAAATAATCT AGTCTTAAAC 8160

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3195 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

ATGAATTCAA ATGGCCATGA GGAGGAGAAG AAGTTGGGGA ATGGAGTTGT GGGGATTCTA 60  
 TCTGAAACAG TTAACAAATG GGAGAGACGA ACACCATTGA CGCCATCGCA TTGCGCTCGC 120  
 CTTTTACACG GTGGGAAAGA CAGAACCGGC ATTTCCCGCA TTGTGGTTCA GCCATCTGCT 180  
 AAGCGTATCC ATCATGATGC CTTGTATGAA CATGTTGGGT GTGAAATTC TGATGATTTG 240  
 TCTGATTGTG GGCTTATACT TGAATCAAA CAACCTGAGC TAGAAATGAT TCTTCCAGAG 300  
 AGAGCATACG CTTTCTTTTC ACATACTCAT AAGGCACAGA AAGAGAACAT GCCTTTGTTG 360  
 GATAAAATTC TTTCTGAGAG AGTGACTTTG TGTGATTATG AGCTCATTGT TGGGGATCAT 420  
 GGGAAACGAT TATTGGCGTT TGGTAAATAT GCAGGCAGAG CTGGTCTTGT TGACTIONT 480  
 CACGGACTTG GACAGCGATA TCTAAGTCTA GGATACTCAA CACCTTTCCT CTCGCTCGGT 540  
 GCATCGTATA TGTATTCCTC ATTGGCTGCT GCAAAGCCG CTGTAATTTT TGTGGTGAA 600  
 GAAATTGCAA GCCAGGGACT GCCATTAGGA ATCTGCCCTC TTGTATTTGT CTTACCCGGA 660  
 ACAGGAAATG TTTCTCTGGG GCGCAAGAA ATTTTCAAGC TTCTTCCTCA CACTTTTGTT 720  
 GAACCAAGCA AACTTCCTGA ACTATTTGTA AAAGACAAAG GAATTAGTCA AAATGGGATT 780  
 TCAACAAAGC GAGTCTATCA AGTATATGGT TGTATTATTA CCAGCCAAGA CATGGTTGAA 840  
 CACAAAGATC CATCAAAGTC ATTCGACAAA GCCGACTATT ATGCACACCC GGAACATTAC 900  
 AATCCAGTTT TCCACGAAAA GATATCGCCA TATACGTCTG TTCTTGTAAC CTGTATGTAC 960  
 TGGGAGAAGA GGTTCCTG TCTTCTGAGC ACAAACAGC TTCAAGATTT AACAAAAAAA 1020  
 GGACTCCCAC TAGTAGGCAT ATGTGATATA ACTTGTGACA TCGGTGGCTC CATTGAATTT 1080  
 GTTAACCGAG CTACTIONTAAAT CGATTCCCCT TTCTTCAGGT TTAATCCCTC GAACAATTCA 1140

TACTACGATG	ACATGGATGG	GGATGGCGTA	CTATGCATGG	CTGTTGACAT	TTTACCCACA	1200
GAATTTGCAA	AAGAGGCATC	CCAGCATTTT	GGAGATATTC	TTTCCGGATT	TGTCGGTAGT	1260
TTGGCTTCAA	TGACTGAAAT	TTCAGATCTA	CCAGCACATC	TGAAGAGGGC	TTGCATAAGC	1320
TATAGGGGAG	AATTGACATC	TTTGTATGAG	TATATTCCAC	GTATGAGGAA	GTCAAATCCA	1380
GAAGAGGCAC	AAGATAATAT	TATCGCCAAC	GGGGTTTCCA	GCCAGAGAAC	ATTCAACATA	1440
TTGGTATCTC	TGAGCGGACA	CCTATTTGAT	AAGTTTCTGA	TAAACGAAGC	TCTTGATATG	1500
ATCGAAGCGG	CTGGTGGCTC	ATTTCATTTG	GCTAAATGTG	AACTGGGGCA	GAGCGCTGAT	1560
GCTGAATCGT	ACTCAGAACT	TGAAGTTGGT	GCGGATGATA	AGAGAGTATT	GGATCAAATC	1620
ATTGATTCAT	TAACTCGGTT	AGCTAATCCA	AATGAAGATT	ATATATCCCC	ACATAGAGAA	1680
GCAAATAAGA	TCTCACTGAA	GATTGGTAAA	GTCCAGCAAG	AAAATGAGAT	AAAAGAGAAG	1740
CCTGAAATGA	CGAAAAAATC	AGGTGTTTTG	ATTCTTGGTG	CTGGACGTGT	GTGTCGCCCC	1800
GCTGCTGATT	TCCTAGCTTC	AGTTAGAACC	ATTTGCTCAC	AGCAATGGTA	CAAAACATAT	1860
TTCGGAGCAG	ACTCTGAAGA	GAAAACAGAT	GTTTCATGTGA	TTGTCGCGTC	TCTGTATCTT	1920
AAGGATGCCA	AAGAGACGGT	TGAAGGTATT	TCAGATGTAG	AAGCAGTTCG	GCTAGATGTA	1980
TCTGATAGTG	AAAGTCTCCT	TAAGTATGTT	TCTCAGGTTG	ATGTTGTCCT	AAGTTTATTA	2040
CCTGCAAGTT	GTCATGCTGT	TGTAGCAAAG	ACATGCATTG	AGCTGAAGAA	GCATCTCGTC	2100
ACTGCTAGCT	ATGTTGATGA	TGAAACGTCC	ATGTTACATG	AGAAGGCTAA	GAGTGCTGGG	2160
ATAACGATTC	TAGGCGAAAT	GGGACTGGAC	CCTGGAATCG	ATCACATGAT	GGCGATGAAA	2220
ATGATCAACG	ATGCTCATAT	CAAAAAGGG	AAAGTGAAGT	CTTTTACCTC	TTATTGTGGA	2280
GGGCTTCCCT	CTCCTGCTGC	AGCAAATAAT	CCATTAGCAT	ATAAATTTAG	CTGGAACCCT	2340
GCTGGAGCAA	TTCGAGCTGG	TCAAAACCCC	GCCAAATACA	AAAGCAACGG	CGACATAATA	2400
CATGTTGATG	GGAAGAATCT	CTATGATTCC	GCGGCAAGAT	TCCGAGTACC	TAATCTTCCA	2460
GCTTTTGCAT	TGGAGTGTTT	TCCAAATCGT	GACTCCTTGG	TTTACGGGGA	ACATTATGGC	2520
ATCGAGAGCG	AAGCAACAAC	GATATTTTCGT	GGAACACTCA	GATATGAAGG	GTTTAGTATG	2580
ATAATGGCAA	CACTTTTCGAA	ACTTGGATTG	TTTGACAGTG	AAGCAAATCA	AGTACTCTCC	2640
ACTGGAAAGA	GGATTACGTT	TGGTGCTCTT	TTAAGTAACA	TTCTAAATAA	GGATGCAGAC	2700
AATGAATCAG	AGCCCCTAGC	GGGAGAAGAA	GAGATAAGCA	AGAGAATTAT	CAAGCTTGGA	2760
CATTCCAAGG	AGACTGCAGC	CAAAGCTGCC	AAAACAATTG	TATTCTTGGG	GTTCAACGAA	2820
GAGAGGGAGG	TTCCATCACT	GTGTAAAAGC	GTATTTGATG	CAACTTGTTA	CCTAATGGAA	2880

GAGAACTAG CTTATTCGG AAATGAACAG GACATGGTGC TTTTGCATCA CGAAGTAGAA 2940  
 GTGGAATTCC TTGAAAGCAA ACGTATAGAG AAGCACACTG CGACTCTTTT GGAATTCGGG 3000  
 GACATCAAGA ATGGACAAAC AACAAACCGCT ATGGCCAAGA CTGTTGGGAT CCCTGCAGCC 3060  
 ATTGGAGCTC TGGTGTAAAT TGAAGACAAG ATCAAGACAA GAGGAGTCTT AAGGCCTCTC 3120  
 GAAGCAGAGG TGTATTTGCC AGCTTTGGAT ATATTGCAAG CATATGGTAT AAAGCTGATG 3180  
 GAGAAGGCAG AATGA 3195

(2) INFORMATION FOR SEQ ID NO:112:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1064 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

Met	Asn	Ser	Asn	Gly	His	Glu	Glu	Glu	Lys	Lys	Leu	Gly	Asn	Gly	Val	1	5	10	15
Val	Gly	Ile	Leu	Ser	Glu	Thr	Val	Asn	Lys	Trp	Glu	Arg	Arg	Thr	Pro	20	25	30	
Leu	Thr	Pro	Ser	His	Cys	Ala	Arg	Leu	Leu	His	Gly	Gly	Lys	Asp	Arg	35	40	45	
Thr	Gly	Ile	Ser	Arg	Ile	Val	Val	Gln	Pro	Ser	Ala	Lys	Arg	Ile	His	50	55	60	
His	Asp	Ala	Leu	Tyr	Glu	His	Val	Gly	Cys	Glu	Ile	Ser	Asp	Asp	Leu	65	70	75	80
Ser	Asp	Cys	Gly	Leu	Ile	Leu	Gly	Ile	Lys	Gln	Pro	Glu	Leu	Glu	Met	85	90	95	
Ile	Leu	Pro	Glu	Arg	Ala	Tyr	Ala	Phe	Phe	Ser	His	Thr	His	Lys	Ala	100	105	110	
Gln	Lys	Glu	Asn	Met	Pro	Leu	Leu	Asp	Lys	Ile	Leu	Ser	Glu	Arg	Val	115	120	125	
Thr	Leu	Cys	Asp	Tyr	Glu	Leu	Ile	Val	Gly	Asp	His	Gly	Lys	Arg	Leu	130	135	140	
Leu	Ala	Phe	Gly	Lys	Tyr	Ala	Gly	Arg	Ala	Gly	Leu	Val	Asp	Phe	Leu	145	150	155	160
His	Gly	Leu	Gly	Gln	Arg	Tyr	Leu	Ser	Leu	Gly	Tyr	Ser	Thr	Pro	Phe	165	170	175	



Leu Ser Leu Gly Ala Ser Tyr Met Tyr Ser Ser Leu Ala Ala Ala Lys  
 180 185 190  
 Ala Ala Val Ile Ser Val Gly Glu Glu Ile Ala Ser Gln Gly Leu Pro  
 195 200 205  
 Leu Gly Ile Cys Pro Leu Val Phe Val Phe Thr Gly Thr Gly Asn Val  
 210 215 220  
 Ser Leu Gly Ala Gln Glu Ile Phe Lys Leu Leu Pro His Thr Phe Val  
 225 230 235 240  
 Glu Pro Ser Lys Leu Pro Glu Leu Phe Val Lys Asp Lys Gly Ile Ser  
 245 250 255  
 Gln Asn Gly Ile Ser Thr Lys Arg Val Tyr Gln Val Tyr Gly Cys Ile  
 260 265 270  
 Ile Thr Ser Gln Asp Met Val Glu His Lys Asp Pro Ser Lys Ser Phe  
 275 280 285  
 Asp Lys Ala Asp Tyr Tyr Ala His Pro Glu His Tyr Asn Pro Val Phe  
 290 295 300  
 His Glu Lys Ile Ser Pro Tyr Thr Ser Val Leu Val Asn Cys Met Tyr  
 305 310 315 320  
 Trp Glu Lys Arg Phe Pro Cys Leu Leu Ser Thr Lys Gln Leu Gln Asp  
 325 330 335  
 Leu Thr Lys Lys Gly Leu Pro Leu Val Gly Ile Cys Asp Ile Thr Cys  
 340 345 350  
 Asp Ile Gly Gly Ser Ile Glu Phe Val Asn Arg Ala Thr Leu Ile Asp  
 355 360 365  
 Ser Pro Phe Phe Arg Phe Asn Pro Ser Asn Asn Ser Tyr Tyr Asp Asp  
 370 375 380  
 Met Asp Gly Asp Gly Val Leu Cys Met Ala Val Asp Ile Leu Pro Thr  
 385 390 395 400  
 Glu Phe Ala Lys Glu Ala Ser Gln His Phe Gly Asp Ile Leu Ser Gly  
 405 410 415  
 Phe Val Gly Ser Leu Ala Ser Met Thr Glu Ile Ser Asp Leu Pro Ala  
 420 425 430  
 His Leu Lys Arg Ala Cys Ile Ser Tyr Arg Gly Glu Leu Thr Ser Leu  
 435 440 445  
 Tyr Glu Tyr Ile Pro Arg Met Arg Lys Ser Asn Pro Glu Glu Ala Gln  
 450 455 460  
 Asp Asn Ile Ile Ala Asn Gly Val Ser Ser Gln Arg Thr Phe Asn Ile  
 465 470 475 480

Leu Val Ser Leu Ser Gly His Leu Phe Asp Lys Phe Leu Ile Asn Glu  
 485 490 495  
 Ala Leu Asp Met Ile Glu Ala Ala Gly Gly Ser Phe His Leu Ala Lys  
 500 505 510  
 Cys Glu Leu Gly Gln Ser Ala Asp Ala Glu Ser Tyr Ser Glu Leu Glu  
 515 520 525  
 Val Gly Ala Asp Asp Lys Arg Val Leu Asp Gln Ile Ile Asp Ser Leu  
 530 535 540  
 Thr Arg Leu Ala Asn Pro Asn Glu Asp Tyr Ile Ser Pro His Arg Glu  
 545 550 555 560  
 Ala Asn Lys Ile Ser Leu Lys Ile Gly Lys Val Gln Gln Glu Asn Glu  
 565 570 575  
 Ile Lys Glu Lys Pro Glu Met Thr Lys Lys Ser Gly Val Leu Ile Leu  
 580 585 590  
 Gly Ala Gly Arg Val Cys Arg Pro Ala Ala Asp Phe Leu Ala Ser Val  
 595 600 605  
 Arg Thr Ile Ser Ser Gln Gln Trp Tyr Lys Thr Tyr Phe Gly Ala Asp  
 610 615 620  
 Ser Glu Glu Lys Thr Asp Val His Val Ile Val Ala Ser Leu Tyr Leu  
 625 630 635 640  
 Lys Asp Ala Lys Glu Thr Val Glu Gly Ile Ser Asp Val Glu Ala Val  
 645 650 655  
 Arg Leu Asp Val Ser Asp Ser Glu Ser Leu Leu Lys Tyr Val Ser Gln  
 660 665 670  
 Val Asp Val Val Leu Ser Leu Leu Pro Ala Ser Cys His Ala Val Val  
 675 680 685  
 Ala Lys Thr Cys Ile Glu Leu Lys Lys His Leu Val Thr Ala Ser Tyr  
 690 695 700  
 Val Asp Asp Glu Thr Ser Met Leu His Glu Lys Ala Lys Ser Ala Gly  
 705 710 715 720  
 Ile Thr Ile Leu Gly Glu Met Gly Leu Asp Pro Gly Ile Asp His Met  
 725 730 735  
 Met Ala Met Lys Met Ile Asn Asp Ala His Ile Lys Lys Gly Lys Val  
 740 745 750  
 Lys Ser Phe Thr Ser Tyr Cys Gly Gly Leu Pro Ser Pro Ala Ala Ala  
 755 760 765  
 Asn Asn Pro Leu Ala Tyr Lys Phe Ser Trp Asn Pro Ala Gly Ala Ile  
 770 775 780

Arg Ala Gly Gln Asn Pro Ala Lys Tyr Lys Ser Asn Gly Asp Ile Ile  
 785 790 795 800  
 His Val Asp Gly Lys Asn Leu Tyr Asp Ser Ala Ala Arg Phe Arg Val  
 805 810 815  
 Pro Asn Leu Pro Ala Phe Ala Leu Glu Cys Phe Pro Asn Arg Asp Ser  
 820 825 830  
 Leu Val Tyr Gly Glu His Tyr Gly Ile Glu Ser Glu Ala Thr Thr Ile  
 835 840 845  
 Phe Arg Gly Thr Leu Arg Tyr Glu Gly Phe Ser Met Ile Met Ala Thr  
 850 855 860  
 Leu Ser Lys Leu Gly Phe Phe Asp Ser Glu Ala Asn Gln Val Leu Ser  
 865 870 875 880  
 Thr Gly Lys Arg Ile Thr Phe Gly Ala Leu Leu Ser Asn Ile Leu Asn  
 885 890 895  
 Lys Asp Ala Asp Asn Glu Ser Glu Pro Leu Ala Gly Glu Glu Ile  
 900 905 910  
 Ser Lys Arg Ile Ile Lys Leu Gly His Ser Lys Glu Thr Ala Ala Lys  
 915 920 925  
 Ala Ala Lys Thr Ile Val Phe Leu Gly Phe Asn Glu Glu Arg Glu Val  
 930 935 940  
 Pro Ser Leu Cys Lys Ser Val Phe Asp Ala Thr Cys Tyr Leu Met Glu  
 945 950 955 960  
 Glu Lys Leu Ala Tyr Ser Gly Asn Glu Gln Asp Met Val Leu Leu His  
 965 970 975  
 His Glu Val Glu Val Glu Phe Leu Glu Ser Lys Arg Ile Glu Lys His  
 980 985 990  
 Thr Ala Thr Leu Leu Glu Phe Gly Asp Ile Lys Asn Gly Gln Thr Thr  
 995 1000 1005  
 Thr Ala Met Ala Lys Thr Val Gly Ile Pro Ala Ala Ile Gly Ala Leu  
 1010 1015 1020  
 Val Leu Ile Glu Asp Lys Ile Lys Thr Arg Gly Val Leu Arg Pro Leu  
 1025 1030 1035 1040  
 Glu Ala Glu Val Tyr Leu Pro Ala Leu Asp Ile Leu Gln Ala Tyr Gly  
 1045 1050 1055  
 Ile Lys Leu Met Glu Lys Ala Glu  
 1060

(2) INFORMATION FOR SEQ ID NO:113:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: modified\_base
  - (B) LOCATION: 6
  - (D) OTHER INFORMATION: /mod\_base=i
- (ix) FEATURE:
  - (A) NAME/KEY: modified\_base
  - (B) LOCATION: 12
  - (D) OTHER INFORMATION: /mod\_base=i
- (ix) FEATURE:
  - (A) NAME/KEY: modified\_base
  - (B) LOCATION: 21
  - (D) OTHER INFORMATION: /mod\_base=i
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

TTYTCNCAYA CNCAYAARGC NCA

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(2) INFORMATION FOR SEQ ID NO:114:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

TTYTCCcart ACATRCartT

20

(2) INFORMATION FOR SEQ ID NO:115:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 619 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

GAAAACATGC CTTTGCTGGA TAAGATTCTA GCTGAGAGGG CATCGTTATA TGACTATGAA

60

TTAATTGTTG GGGACACTGG GAAAAGGTTA CTTGCATTTG GAAAATTCGC TGGTAGGGCT

120

GGAATGATCG ACTTTTTGCG CGGATTAGGA CAGCGGTTTT TAAGTCTTGG ATATTCAACA	180
CCTTCTTGT CACTTGGATC ATCTTACATG TACCCTTCCC TGGCTGCTGC TAAGGCTGCT	240
GTGATTTCTG TTGGTGAAAA ATTGCGACGC AGGGATTGCC ATTGGGGATT TGTCCCCTGG	300
TTTGTTTATT TACTGGTTCA GGAAATGTTT GTTCTGGTGC ACAGGAGATA TTTAAGCTTC	360
TTCTCATAC CTTTGTTGAT CCATCTAAAC TACGCGACCT ACATAGAACG GACCCAGATC	420
AACCAAGGCA TGCTTCAAAA AGAGTTTTC AAGTTTATGG TTGTGTTGTG ACTGCCCAAG	480
ACATGGTTGA ACCCAAAGAT CACGTGATAG TGTTTGACAA AGCAGACTAC TATGCACATC	540
CTGAGCATT CAATCCCACT TTCCATGAAA AAATAGCACC ATATGCATCT GTTATTGTCA	600
ATTGCATGTA TTGGGAAAA	619

(2) INFORMATION FOR SEQ ID NO:116:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 620 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

GAGAATATGC CACTGTTAGA CAAGATCCTT GAAGAAAGGG TGCCTTGTT TGATTATGAG	60
CTAATTGTTG GAGATGATGG GAAAAGATCA CTAGCATTTG GGAAATTTGC TGGTAGAGCT	120
GGACTGATAG ATTTCTTACA TGGTCTCGGA CAGCGATATT TGAGCCTTGG ATACTCCACT	180
CCATTTCTCT CTCTGGGACA TCTCATATGT TCCTTCGCTC GCTGCAGCCA AGGCTGCAGT	240
CATTGTCGTT GCAGAAGAGA TAGCAACATT TGGACTTCCA TCCGGAATTT GTCCGATAGT	300
GTTTGTGTTT ACTGGAGTTG GAAACGTCTC TCAGGGTGCG CAGGAGATAT TCAAGTTATT	360
GCCCCATACC TTTGTTGATG CTGAGAAGCT TCCCGAAATT TTTCAGGCCA GGAATCTGTC	420
TAAGCAATCT CAGTCGACCA AGAGAGTATT TCAACTTTAT GGTTGTGTTG TGACCTCTAG	480
AGACATAGTT TCTCACAAGG ATCCCACCAG ACAATTTGAC AAAGGTGACT ATTATGCTCA	540
TCCAGAACAC TACACCCCTG TTTTTCATGA AAGAATTGCT CCATATGCAT CTGTCATCGT	600
AAACTGCATG TATTGGGAAA	620

(2) INFORMATION FOR SEQ ID NO:117:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 206 amino acids
  - (B) TYPE: amino acid

(C) STRANDEDNESS: unknown

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

Glu Asn Met Pro Leu Leu Asp Lys Ile Leu Ala Glu Arg Ala Ser Leu  
1                   5                   10                   15  
Tyr Asp Tyr Glu Leu Ile Val Gly Asp Thr Gly Lys Arg Leu Leu Ala  
20                   25                   30  
Phe Gly Lys Phe Ala Gly Arg Ala Gly Met Ile Asp Phe Leu Arg Gly  
35                   40                   45  
Leu Gly Gln Arg Phe Leu Ser Leu Gly Tyr Ser Thr Pro Phe Leu Ser  
50                   55                   60  
Leu Gly Ser Ser Tyr Met Tyr Pro Ser Leu Ala Ala Ala Lys Ala Ala  
65                   70                   75                   80  
Val Ile Ser Val Gly Glu Xaa Ile Ala Thr Gln Gly Leu Pro Leu Gly  
85                   90                   95  
Ile Cys Pro Leu Val Cys Leu Phe Thr Gly Ser Gly Asn Val Cys Ser  
100                   105                   110  
Gly Ala Gln Glu Ile Phe Lys Leu Leu Pro His Thr Phe Val Asp Pro  
115                   120                   125  
Ser Lys Leu Arg Asp Leu His Arg Thr Asp Pro Asp Gln Pro Arg His  
130                   135                   140  
Ala Ser Lys Arg Val Phe Gln Val Tyr Gly Cys Val Val Thr Ala Gln  
145                   150                   155                   160  
Asp Met Val Glu Pro Lys Asp His Val Ile Val Phe Asp Lys Ala Asp  
165                   170                   175  
Tyr Tyr Ala His Pro Glu His Tyr Asn Pro Thr Phe His Glu Lys Ile  
180                   185                   190  
Ala Pro Tyr Ala Ser Val Ile Val Asn Cys Met Tyr Trp Glu  
195                   200                   205

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 207 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: unknown

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

Glu	Asn	Met	Pro	Leu	Leu	Asp	Lys	Ile	Leu	Glu	Glu	Arg	Val	Ser	Leu	1	5	10	15
Phe	Asp	Tyr	Glu	Leu	Ile	Val	Gly	Asp	Asp	Gly	Lys	Arg	Ser	Leu	Ala	20	25	30	
Phe	Gly	Lys	Phe	Ala	Gly	Arg	Ala	Gly	Leu	Ile	Asp	Phe	Leu	His	Gly	35	40	45	
Leu	Gly	Gln	Arg	Tyr	Leu	Ser	Leu	Gly	Tyr	Ser	Thr	Pro	Phe	Leu	Ser	50	55	60	
Leu	Gly	Xaa	Ser	His	Met	Xaa	Pro	Ser	Leu	Ala	Ala	Ala	Lys	Ala	Ala	65	70	75	80
Val	Ile	Val	Val	Ala	Glu	Glu	Ile	Ala	Thr	Phe	Gly	Leu	Pro	Ser	Gly	85	90	95	
Ile	Cys	Pro	Ile	Val	Phe	Val	Phe	Thr	Gly	Val	Gly	Asn	Val	Ser	Gln	100	105	110	
Gly	Ala	Gln	Glu	Ile	Phe	Lys	Leu	Leu	Pro	His	Thr	Phe	Val	Asp	Ala	115	120	125	
Glu	Lys	Leu	Pro	Glu	Ile	Phe	Gln	Ala	Arg	Asn	Leu	Ser	Lys	Gln	Ser	130	135	140	
Gln	Ser	Thr	Lys	Arg	Val	Phe	Gln	Leu	Tyr	Gly	Cys	Val	Val	Thr	Ser	145	150	155	160
Arg	Asp	Ile	Val	Ser	His	Lys	Asp	Pro	Thr	Arg	Gln	Phe	Asp	Lys	Gly	165	170	175	
Asp	Tyr	Tyr	Ala	His	Pro	Glu	His	Tyr	Thr	Pro	Val	Phe	His	Glu	Arg	180	185	190	
Ile	Ala	Pro	Tyr	Ala	Ser	Val	Ile	Val	Asn	Cys	Met	Tyr	Trp	Glu	195	200	205		

(2) INFORMATION FOR SEQ ID NO:119:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2582 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Glycine max
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 3..2357

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

TTGAACCCAA	AGATCACGTG	ATAGTGTGTTG	ACAAAGCAGA	CTACTATTCA	CACCCTGAGC	60
ATTACAATCC	CACTTTCCAT	GAAAAAATAG	CACCATATGC	ATCTGTTATT	GTCAATTGCA	120
TGTATTGGGA	GAAAAGATTT	CCTCAATTGC	CGAGCTATAA	GCAGATGCAA	GACTTAATGG	180
GCCGGGGGAG	CCCCCTTGTT	GGAATAGCTG	ACATAACGTG	TGATATAGGG	GGTTCAATTG	240
AGTTTGTTAA	CCGCGGTACT	TCAATTGATT	CACCCTTCTT	CAGATATGAT	CCCTTAACAA	300
ATTCCTACCA	TGATGATATG	GAGGGGAATG	GAGTGATATG	CTTAGCTGTT	GACATTCTTC	360
CAACAGAATT	TGCAAAGGAG	GCTTCCCAAC	ATTTTGGAAG	CATACTTTCC	CAATTTGTTG	420
TAAATTTGGC	TTCTGCTACA	GACATTACAA	AGTTGCCTGC	TCACTTAAGG	AGAGCTTGCA	480
TAGCCCATAA	AGGAGTGCTA	ACCTCCTTAT	ATGATTATAT	CCCACGCATG	CGGAGTTCTG	540
ATTCAGAGGA	AGTATCAGAA	AACGCAGAAA	ATTCTCTATC	CAACAAAAGG	AAGTACAATA	600
TATCGGTGTC	TCTGAGTGGT	CACTTATTTG	ATCAGTTTCT	GATAAATGAG	GCCTTAGATA	660
TTATTGAAGC	TGCAGGAGGC	TCCTTCCACT	TAGTCAACTG	CCATGTGGGT	CAGAGCATTG	720
AAGCCGTATC	ATTCTCTGAA	CTTGAAGTTG	GTGCAGATAA	CAGGGCTGTT	CTGGATCAAA	780
TCATTGATTC	TTTAACTGCT	ATTGCTAGTC	CAACTGAACA	TGATAGATTT	TCAAATCAAG	840
ATTCAAGTAA	AATTTCACTT	AAGCTTGGTA	AAGTTGAAGA	GAATGGCATA	GAGAAGGAAT	900
CTGACCCAG	AAAGAAGGCT	GCGGTTTTAA	TTCTTGAGGC	TGGTCGGGTC	TGTCAACCAG	960
CTGCTGAAAT	GTTATCATCA	TTTGAAGGC	CATCATCGAG	CCAATGGTAT	AAAACATTGT	1020
TGGAAGATGA	TTTTGAATGT	CAAACGTATG	TAGAAGTCAT	TGTGGGATCT	CTGTACCTGA	1080
AGGATGCAGA	GCAGACTGTT	GAGGGCATTG	CAAATGTAAC	CGGAATTCAG	CTTGATGTGA	1140
TGGATCGTGC	CAATTTGTGT	AAGTACATTT	CACAGGTTGA	CGTTGTTATA	AGTTTGCTGC	1200
CCCCAAGTTG	TCATATTATT	GTAGCAAATG	CTTGCAATTG	GCTGAAAAAA	CATCTTGTCA	1260
CTGCTAGCTA	TGTTGATAGC	TCCATGTCAA	TGCTAAATGA	TAAGGCTAAA	GATGCTGGCA	1320
TAACAATTCT	TGGAGAGATG	GGCTTGGACC	CAGGAATTGG	TCATATGATG	GCAATGAAGA	1380
TGATCAACCA	AGCACATGTG	AGGAAGGGGA	AAATAAAGTC	TTTCACTTCT	TATTGTGGTG	1440
GACTTCCATC	TCCTGAAGCT	GCTAACAATC	CATTAGCATA	TAAATTCAGT	TGGAATCCTG	1500
CAGGAGCCAT	CCGAGCTGGG	CGCAATCCTG	CCACCTACAA	ATGGGGTGGT	GAAACTGTAC	1560
ATATTGATGG	GGACGATCTT	TATGATTCGG	CTACAAGACT	AAGGCTACCG	GACCTTCCTG	1620
CTTTTGCTTT	GGAATGTCTC	CCAAATCGCA	ATTCATTACT	TTATGGGGAT	TTGTATGGAA	1680
TAACTGAAGC	ATCAACCATT	TTCCGTGGAA	CCCTCCGCTA	TGAAGGATTT	AGTGAGATCA	1740
TGGGGACACT	GTCTAGGATT	AGCTTATTTA	ACAATGAAGC	CCATTTCGTT	CTAATGAATG	1800
GACAAAGACC	AACTTTCAAA	AAATTCTTAT	TTGAACTTCT	CAAAGTTGTT	GGTGATAATC	1860



CAGATGAACT ATTGATAGGA GAGAATGACA TCATGGAGCA AATATTAATA CAAGGGCACT 1920  
 GCAAAGATCA AAGAACGGCA ATGGAGACAG CAAAAACAAT CATTTTCTTG GGACTTCTTG 1980  
 ACCAAACTGA AATCCCTGCT TCCTGCAAAA GTGCTTTTGA TGTTGCTTGT TTCCGCATGG 2040  
 AGGAGAGGTT ATCATACACC AGCACAGAAA AGGATATGGT GCTTTTGCAT CATGAAGTGG 2100  
 AAATAGAATA CCCAGATAGC CAAATTACAG AGAAGCATAG AGCTACTTTA CTTGAATTTG 2160  
 GGAAGACTCT TGATGAAAAA ACCACAACCTG CCATGGCCCT TACTGTTGGT ATTCCAGCTG 2220  
 CTGTTGGAGC TTTGCTTTTA TTGACAAACA AAATTCAGAC AAGAGGAGTC TTAAGGCCTA 2280  
 TCGAACCTGA AGTATACAAT CCAGCACTGG ATATTATAGA AGCTTATGGG ATCAAGTTGA 2340  
 TAGAGAAGAC CGAGTAATTT GCATYTATGA ATTGATGTAT AGGTGTACAT TAATGTACAC 2400  
 CATGCAATGT TTGATTTGAA TAAGATAAAA TATAATAATT ACTGCAGTCA TGAATTTGCA 2460  
 ACTGCCATTC TATGCAACTG TCAGAAATGG ACCACACGGT ACCAGCATAG TTAACAACT 2520  
 TAGGCAGATA CCAATTTCAA TTGCAGCAGT ACAATCCAAC CAGTTATGAA GTATGGTTCT 2580  
 AG 2582

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 3265 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Zea mays

(ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 3..3071

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

ATTGTGCCCCG CCTTCTGCTA GGAGGAGGCA AGAACGGACC TCGAGTAAAC CGGATTATTG 60  
 TGCAGCCAAG CACAAGGAGG ATCCATCATG ACGCTCAGTA TGAGGATGCA GGATGCGAGA 120  
 TTTTCAAGA CCTGTCAGAA TGCGGCCTTA TCATAGGCAT CAAACAACCC AAGCTGCAGA 180  
 TGATTCTTTC AGATAGAGCG TACGCTTTCT TTTACACAC ACACAAAGCC CAAAAGAGA 240  
 ATATGCCACT GTTAGACAAG ATCCTTGAAG AAAGGGTGTC CTTGTTTGAT TATGAGCTAA 300  
 TTGTTGGAGA TGATGGGAAA AGATCACTAG CATTTGGGAA ATTTGCTGGT AGAGCTGGAC 360  
 TGATAGATTT CTTACATGGT CTCGGACAGC GATATTTGAG CCTTGGATAC TCGACTCCAT 420  
 TTCTCTCTCT GGGACAATCT CATATGTATC CTTGCTCGC TGCAGCCAAG GCTGCAGTCA 480

TTGTCGTTGC	AGAAGAGATA	GCAACATTTG	GACTTCCATC	CGGAATTTGT	CCGATAGTGT	540
TTGTGTTTAC	TGGAGTTGGA	AACGTCTCTC	AGGGTGCGCA	GGAGATATTC	AAGTTATTGC	600
CCCATACCTT	TGTTGATGCT	GAGAAGCTTC	CCGAAATTTT	TCAGGCCAGG	AATCTGTCTA	660
AGCAATCTCA	GTCGACCAAG	AGAGTATTTT	AACTTTATGG	TTGTGTTGTG	ACCTCTAGAG	720
ACATAGTTTC	TCACAAGGAT	CCCACCAGAC	AATTTGACAA	AGGTGACTAT	TATGCTCATC	780
CAGAACACTA	CACCCCTGTT	TTTCATGAAA	GAATTGCTCC	ATATGCATCT	GTCATCGTAA	840
ACTGTATGTA	TTGGGAGAAG	AGGTTTCCAC	CATTACTAAA	TATGGATCAG	TTACAGCAAT	900
TGATGGAGAC	TGTTTGTCTT	TTAGTCGGCG	TTTGTGACAT	AACTTGTGAT	ATTGGAGGTT	960
CCATTGAATT	TATCAACAAG	AGTACATCAA	TAGAGAGGCC	TTTCTTTCGG	TATGATCCTT	1020
CTAAGAATTC	ATACCATGAT	GATATGGAAG	GTGCCGGAGT	GGTCTGCTTG	GCTGTTGACA	1080
TTCTCCCTAC	AGAATTCTCT	AAAGAGGCCT	CCCAACATTT	TGGAAACATA	CTATCTAGAC	1140
TTGTTGCTAG	TTTGGCCTCA	GTGAAGCAAC	CGGCAGAACT	TCCTTCCTAC	TTGAGAAGAG	1200
CTTGCAATTGC	ACATGCTGGC	AGATTAACTC	CTTTGTATGA	ATATATCCCT	AGGATGAGAA	1260
ATACTATGAT	AGATTTGGCA	CCCGCAAAAA	CAAATCCATT	GCCTGACAAG	AAGTATAGCA	1320
CCCTGGTATC	TCTCAGTGGG	CACCTATTTG	ATAAGTTCCT	TATAAATGAA	GCTTTGGACA	1380
TCATTGAGAC	AGCTGGAGGT	TCATTTCACT	TGGTTAGATG	TGAAGTTGGA	CAAAGCACGG	1440
ATGATATGTC	ATACTCAGAG	CTTGAAGTAG	GAGCAGATGA	TACTGCCACA	TTGGATAAAA	1500
TTATTGATTC	CTTGACTTCT	TTAGCTAATG	AACATGGTGG	AGATCACGAT	GCCGGGCAAG	1560
AAATTGAATT	AGCTCTGAAG	ATAGGAAAAG	TCAATGAGTA	TGAAACTGAC	GTCACAATTG	1620
ATAAAGGAGG	GCCAAAGATT	TTAATTCTTG	GAGCTGGAAG	AGTCTGTGCG	CCAGCTGCTG	1680
AGTTTCTGGC	ATCTTACCCA	GACATATGTA	CCTATGGTGT	TGATGACCAT	GATGCAGATC	1740
AAATTCATGT	TATCGTGGCA	TCTTTGTATC	AAAAAGATGC	AGAAGAGACA	GTTGATGGTA	1800
TTGAAAATAC	AACTGCTACC	CAGCTTGATG	TTGCTGATAT	TGGAAGCCTT	TCAGATCTTG	1860
TTTCTCAGGT	TGAGGTTGTA	ATTAGCTTGC	TGCCTGCTAG	TTTTCATGCT	GCCATTGCAG	1920
GAGTATGCAT	AGAGTTGAAG	AAGCACATGG	TAACGGCAAG	CTATGTTGAT	GAATCCATGT	1980
CAAACCTTGAG	CCAAGCTGCC	AAAGATGCAG	GTGTAACAT	ACTTTGTGAA	ATGGGCCTAG	2040
ATCCTGGCAT	AGATCACTTG	ATGTCAATGA	AGATGATTGA	TGAAGCTCAT	GCACGAAAGG	2100
GAAAAATAAA	GGCATTTACA	TCTTACTGTG	GTGGATTGCC	ATCTCCAGCT	GCAGCAAACA	2160
ATCCGCTTGC	CTATAAATTC	AGTTGGAACC	CAGCTGGTGC	ACTCCGGTCA	GGGAAAAATC	2220
CTGCAGTCTA	CAAATTTCTT	GGTGAGACGA	TCCATGTAGA	TGGTCATAAC	TTGTATGAAT	2280
CAGCAAAGAG	GCTCAGACTA	CGAGAGCTTC	CAGCTTTTGC	TCTGGAACAC	TTGCCAAATC	2340
GGAATTCCTT	GATATATGGT	GACCTTTATG	GTATCTCCAA	AGAAGCATCC	ACCATATATA	2400

GGGCTACTYT TCGTTACGAA GGTTTTAGTG AGATTATGGT AACCCCTTCC AAAACTGGGT 2460  
 TCTTTGATGC TGCAAATCAT CCACTGCTGC AAGATACTAG TCGTCCAACA TATAAGGGTT 2520  
 TCCTTGATGA ACTACTGAAT AATATCTCCA CAATTAACAC GGACTTAGAT ATTGAAGCTT 2580  
 CTGGTGGATA CGATGATGAC CTGATTGCCA GACTGTTGAA GCTCGGGTGT TGCAAAAATA 2640  
 AGGAAATAGC TGTTAAGACA GTCAAAACCA TCAAGTTCTT GGGACTACAT GAAGAGACTC 2700  
 AAATACCTAA GGGTTGTTTC AGCCCATTTG ATGTGATTTG CCAGCGAATG GAACAGAGGA 2760  
 TGGCCTATGG CCACAATGAG CAAGACATGG TACTGCTCCA CCACGAAGTC GAGGTGGAAT 2820  
 ACCCGGACGG GCAACCCGCC GAAAAGCACC AAGCGACGCT ACTGGAGTTC GGGAAAGTTG 2880  
 AAAATGGCAG GTCCACCACT GCCATGGCGC TGACCGTCGG CATTCCAGCA GCAATAGGGG 2940  
 CCCTGCTATT GCTAAAGAAT AAGGTCCAGA CGAAAGGAGT GATCAGGCCT CTGCAACCGG 3000  
 AAATCTACGT TCCAGCATTG GAGATCTTGG AGTCGTCGGG CATCAAGCTG GTTGAGAAAG 3060  
 TGGAGACTTG AAAGTTCCCT GATACACAGA TAAAGATAGT ATGATATAGC AGGGCACATG 3120  
 TATCTTTTGT ATTAACCTCCG TTCTGGAATA TATATTTGTG AACTAAAATG TGACAAATAA 3180  
 AAAGAACGGG TGGAGTATAT TGTAAGAGAC GGCAAAGAAA CCTCTGTATA TATGACCTGT 3240  
 CGATATCAAA TAATGCCGAT CAGTT 3265

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 784 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Glycine max

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

Glu	Pro	Lys	Asp	His	Val	Ile	Val	Phe	Asp	Lys	Ala	Asp	Tyr	Tyr	Ser
1				5					10					15	
His	Pro	Glu	His	Tyr	Asn	Pro	Thr	Phe	His	Glu	Lys	Ile	Ala	Pro	Tyr
			20					25					30		
Ala	Ser	Val	Ile	Val	Asn	Cys	Met	Tyr	Trp	Glu	Lys	Arg	Phe	Pro	Gln
		35					40					45			
Leu	Pro	Ser	Tyr	Lys	Gln	Met	Gln	Asp	Leu	Met	Gly	Arg	Gly	Ser	Pro
	50					55					60				
Leu	Val	Gly	Ile	Ala	Asp	Ile	Thr	Cys	Asp	Ile	Gly	Gly	Ser	Ile	Glu
65					70					75				80	

Phe Val Asn Arg Gly Thr Ser Ile Asp Ser Pro Phe Phe Arg Tyr Asp  
85 90 95  
Pro Leu Thr Asn Ser Tyr His Asp Asp Met Glu Gly Asn Gly Val Ile  
100 105 110  
Cys Leu Ala Val Asp Ile Leu Pro Thr Glu Phe Ala Lys Glu Ala Ser  
115 120 125  
Gln His Phe Gly Asn Ile Leu Ser Gln Phe Val Val Asn Leu Ala Ser  
130 135 140  
Ala Thr Asp Ile Thr Lys Leu Pro Ala His Leu Arg Arg Ala Cys Ile  
145 150 155 160  
Ala His Lys Gly Val Leu Thr Ser Leu Tyr Asp Tyr Ile Pro Arg Met  
165 170 175  
Arg Ser Ser Asp Ser Glu Glu Val Ser Glu Asn Ala Glu Asn Ser Leu  
180 185 190  
Ser Asn Lys Arg Lys Tyr Asn Ile Ser Val Ser Leu Ser Gly His Leu  
195 200 205  
Phe Asp Gln Phe Leu Ile Asn Glu Ala Leu Asp Ile Ile Glu Ala Ala  
210 215 220  
Gly Gly Ser Phe His Leu Val Asn Cys His Val Gly Gln Ser Ile Glu  
225 230 235 240  
Ala Val Ser Phe Ser Glu Leu Glu Val Gly Ala Asp Asn Arg Ala Val  
245 250 255  
Leu Asp Gln Ile Ile Asp Ser Leu Thr Ala Ile Ala Ser Pro Thr Glu  
260 265 270  
His Asp Arg Phe Ser Asn Gln Asp Ser Ser Lys Ile Ser Leu Lys Leu  
275 280 285  
Gly Lys Val Glu Glu Asn Gly Ile Glu Lys Glu Ser Asp Pro Arg Lys  
290 295 300  
Lys Ala Ala Val Leu Ile Leu Gly Ala Gly Arg Val Cys Gln Pro Ala  
305 310 315 320  
Ala Glu Met Leu Ser Ser Phe Gly Arg Pro Ser Ser Ser Gln Trp Tyr  
325 330 335  
Lys Thr Leu Leu Glu Asp Asp Phe Glu Cys Gln Thr Asp Val Glu Val  
340 345 350  
Ile Val Gly Ser Leu Tyr Leu Lys Asp Ala Glu Gln Thr Val Glu Gly  
355 360 365  
Ile Pro Asn Val Thr Gly Ile Gln Leu Asp Val Met Asp Arg Ala Asn  
370 375 380  
Leu Cys Lys Tyr Ile Ser Gln Val Asp Val Val Ile Ser Leu Leu Pro  
385 390 395 400  
Pro Ser Cys His Ile Ile Val Ala Asn Ala Cys Ile Glu Leu Lys Lys  
405 410 415  
His Leu Val Thr Ala Ser Tyr Val Asp Ser Ser Met Ser Met Leu Asn  
420 425 430

Asp Lys Ala Lys Asp Ala Gly Ile Thr Ile Leu Gly Glu Met Gly Leu  
 435 440 445  
 Asp Pro Gly Ile Gly His Met Met Ala Met Lys Met Ile Asn Gln Ala  
 450 455 460  
 His Val Arg Lys Gly Lys Ile Lys Ser Phe Thr Ser Tyr Cys Gly Gly  
 465 470 475 480  
 Leu Pro Ser Pro Glu Ala Ala Asn Asn Pro Leu Ala Tyr Lys Phe Ser  
 485 490 495  
 Trp Asn Pro Ala Gly Ala Ile Arg Ala Gly Arg Asn Pro Ala Thr Tyr  
 500 505 510  
 Lys Trp Gly Gly Glu Thr Val His Ile Asp Gly Asp Asp Leu Tyr Asp  
 515 520 525  
 Ser Ala Thr Arg Leu Arg Leu Pro Asp Leu Pro Ala Phe Ala Leu Glu  
 530 535 540  
 Cys Leu Pro Asn Arg Asn Ser Leu Leu Tyr Gly Asp Leu Tyr Gly Ile  
 545 550 555 560  
 Thr Glu Ala Ser Thr Ile Phe Arg Gly Thr Leu Arg Tyr Glu Gly Phe  
 565 570 575  
 Ser Glu Ile Met Gly Thr Leu Ser Arg Ile Ser Leu Phe Asn Asn Glu  
 580 585 590  
 Ala His Ser Leu Leu Met Asn Gly Gln Arg Pro Thr Phe Lys Lys Phe  
 595 600 605  
 Leu Phe Glu Leu Leu Lys Val Val Gly Asp Asn Pro Asp Glu Leu Leu  
 610 615 620  
 Ile Gly Glu Asn Asp Ile Met Glu Gln Ile Leu Ile Gln Gly His Cys  
 625 630 635 640  
 Lys Asp Gln Arg Thr Ala Met Glu Thr Ala Lys Thr Ile Ile Phe Leu  
 645 650 655  
 Gly Leu Leu Asp Gln Thr Glu Ile Pro Ala Ser Cys Lys Ser Ala Phe  
 660 665 670  
 Asp Val Ala Cys Phe Arg Met Glu Glu Arg Leu Ser Tyr Thr Ser Thr  
 675 680 685  
 Glu Lys Asp Met Val Leu Leu His His Glu Val Glu Ile Glu Tyr Pro  
 690 695 700  
 Asp Ser Gln Ile Thr Glu Lys His Arg Ala Thr Leu Leu Glu Phe Gly  
 705 710 715 720  
 Lys Thr Leu Asp Glu Lys Thr Thr Thr Ala Met Ala Leu Thr Val Gly  
 725 730 735  
 Ile Pro Ala Ala Val Gly Ala Leu Leu Leu Thr Asn Lys Ile Gln  
 740 745 750  
 Thr Arg Gly Val Leu Arg Pro Ile Glu Pro Glu Val Tyr Asn Pro Ala  
 755 760 765  
 Leu Asp Ile Ile Glu Ala Tyr Gly Ile Lys Leu Ile Glu Lys Thr Glu

## (2) INFORMATION FOR SEQ ID NO:122:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1022 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Zea mays

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

Cys Ala Arg Leu Leu Leu Gly Gly Gly Lys Asn Gly Pro Arg Val Asn  
 1 5 10 15  
 Arg Ile Ile Val Gln Pro Ser Thr Arg Arg Ile His His Asp Ala Gln  
 20 25 30  
 Tyr Glu Asp Ala Gly Cys Glu Ile Ser Glu Asp Leu Ser Glu Cys Gly  
 35 40 45  
 Leu Ile Ile Gly Ile Lys Gln Pro Lys Leu Gln Met Ile Leu Ser Asp  
 50 55 60  
 Arg Ala Tyr Ala Phe Phe Ser His Thr His Lys Ala Gln Lys Glu Asn  
 65 70 75 80  
 Met Pro Leu Leu Asp Lys Ile Leu Glu Glu Arg Val Ser Leu Phe Asp  
 85 90 95  
 Tyr Glu Leu Ile Val Gly Asp Asp Gly Lys Arg Ser Leu Ala Phe Gly  
 100 105 110  
 Lys Phe Ala Gly Arg Ala Gly Leu Ile Asp Phe Leu His Gly Leu Gly  
 115 120 125  
 Gln Arg Tyr Leu Ser Leu Gly Tyr Ser Thr Pro Phe Leu Ser Leu Gly  
 130 135 140  
 Gln Ser His Met Tyr Pro Ser Leu Ala Ala Ala Lys Ala Ala Val Ile  
 145 150 155 160  
 Val Val Ala Glu Glu Ile Ala Thr Phe Gly Leu Pro Ser Gly Ile Cys  
 165 170 175  
 Pro Ile Val Phe Val Phe Thr Gly Val Gly Asn Val Ser Gln Gly Ala  
 180 185 190  
 Gln Glu Ile Phe Lys Leu Leu Pro His Thr Phe Val Asp Ala Glu Lys  
 195 200 205  
 Leu Pro Glu Ile Phe Gln Ala Arg Asn Leu Ser Lys Gln Ser Gln Ser  
 210 215 220  
 Thr Lys Arg Val Phe Gln Leu Tyr Gly Cys Val Val Thr Ser Arg Asp  
 225 230 235 240  
 Ile Val Ser His Lys Asp Pro Thr Arg Gln Phe Asp Lys Gly Asp Tyr

245						250						255			
Tyr	Ala	His	Pro	Glu	His	Tyr	Thr	Pro	Val	Phe	His	Glu	Arg	Ile	Ala
			260					265					270		
Pro	Tyr	Ala	Ser	Val	Ile	Val	Asn	Cys	Met	Tyr	Trp	Glu	Lys	Arg	Phe
		275				280						285			
Pro	Pro	Leu	Leu	Asn	Met	Asp	Gln	Leu	Gln	Gln	Leu	Met	Glu	Thr	Gly
	290					295					300				
Cys	Pro	Leu	Val	Gly	Val	Cys	Asp	Ile	Thr	Cys	Asp	Ile	Gly	Gly	Ser
305				310						315					320
Ile	Glu	Phe	Ile	Asn	Lys	Ser	Thr	Ser	Ile	Glu	Arg	Pro	Phe	Phe	Arg
				325					330					335	
Tyr	Asp	Pro	Ser	Lys	Asn	Ser	Tyr	His	Asp	Asp	Met	Glu	Gly	Ala	Gly
			340					345					350		
Val	Val	Cys	Leu	Ala	Val	Asp	Ile	Leu	Pro	Thr	Glu	Phe	Ser	Lys	Glu
		355				360						365			
Ala	Ser	Gln	His	Phe	Gly	Asn	Ile	Leu	Ser	Arg	Leu	Val	Ala	Ser	Leu
	370					375					380				
Ala	Ser	Val	Lys	Gln	Pro	Ala	Glu	Leu	Pro	Ser	Tyr	Leu	Arg	Arg	Ala
385					390					395					400
Cys	Ile	Ala	His	Ala	Gly	Arg	Leu	Thr	Pro	Leu	Tyr	Glu	Tyr	Ile	Pro
				405					410					415	
Arg	Met	Arg	Asn	Thr	Met	Ile	Asp	Leu	Ala	Pro	Ala	Lys	Thr	Asn	Pro
			420					425					430		
Leu	Pro	Asp	Lys	Lys	Tyr	Ser	Thr	Leu	Val	Ser	Leu	Ser	Gly	His	Leu
		435				440						445			
Phe	Asp	Lys	Phe	Leu	Ile	Asn	Glu	Ala	Leu	Asp	Ile	Ile	Glu	Thr	Ala
	450					455					460				
Gly	Gly	Ser	Phe	His	Leu	Val	Arg	Cys	Glu	Val	Gly	Gln	Ser	Thr	Asp
465					470					475					480
Asp	Met	Ser	Tyr	Ser	Glu	Leu	Glu	Val	Gly	Ala	Asp	Asp	Thr	Ala	Thr
				485					490					495	
Leu	Asp	Lys	Ile	Ile	Asp	Ser	Leu	Thr	Ser	Leu	Ala	Asn	Glu	His	Gly
			500					505					510		
Gly	Asp	His	Asp	Ala	Gly	Gln	Glu	Ile	Glu	Leu	Ala	Leu	Lys	Ile	Gly
		515					520					525			
Lys	Val	Asn	Glu	Tyr	Glu	Thr	Asp	Val	Thr	Ile	Asp	Lys	Gly	Gly	Pro
	530					535					540				
Lys	Ile	Leu	Ile	Leu	Gly	Ala	Gly	Arg	Val	Cys	Arg	Pro	Ala	Ala	Glu
545					550					555					560
Phe	Leu	Ala	Ser	Tyr	Pro	Asp	Ile	Cys	Thr	Tyr	Gly	Val	Asp	Asp	His
				565					570					575	
Asp	Ala	Asp	Gln	Ile	His	Val	Ile	Val	Ala	Ser	Leu	Tyr	Gln	Lys	Asp
			58												

Ala Glu Glu Thr Val Asp Gly Ile Glu Asn Thr Thr Ala Thr Gln Leu  
 595 600 605  
 Asp Val Ala Asp Ile Gly Ser Leu Ser Asp Leu Val Ser Gln Val Glu  
 610 615 620  
 Val Val Ile Ser Leu Leu Pro Ala Ser Phe His Ala Ala Ile Ala Gly  
 625 630 635 640  
 Val Cys Ile Glu Leu Lys Lys His Met Val Thr Ala Ser Tyr Val Asp  
 645 650 655  
 Glu Ser Met Ser Asn Leu Ser Gln Ala Ala Lys Asp Ala Gly Val Thr  
 660 665 670  
 Ile Leu Cys Glu Met Gly Leu Asp Pro Gly Ile Asp His Leu Met Ser  
 675 680 685  
 Met Lys Met Ile Asp Glu Ala His Ala Arg Lys Gly Lys Ile Lys Ala  
 690 695 700  
 Phe Thr Ser Tyr Cys Gly Gly Leu Pro Ser Pro Ala Ala Ala Asn Asn  
 705 710 715 720  
 Pro Leu Ala Tyr Lys Phe Ser Trp Asn Pro Ala Gly Ala Leu Arg Ser  
 725 730 735  
 Gly Lys Asn Pro Ala Val Tyr Lys Phe Leu Gly Glu Thr Ile His Val  
 740 745 750  
 Asp Gly His Asn Leu Tyr Glu Ser Ala Lys Arg Leu Arg Leu Arg Glu  
 755 760 765  
 Leu Pro Ala Phe Ala Leu Glu His Leu Pro Asn Arg Asn Ser Leu Ile  
 770 775 780  
 Tyr Gly Asp Leu Tyr Gly Ile Ser Lys Glu Ala Ser Thr Ile Tyr Arg  
 785 790 795 800  
 Ala Thr Xaa Arg Tyr Glu Gly Phe Ser Glu Ile Met Val Thr Leu Ser  
 805 810 815  
 Lys Thr Gly Phe Phe Asp Ala Ala Asn His Pro Leu Leu Gln Asp Thr  
 820 825 830  
 Ser Arg Pro Thr Tyr Lys Gly Phe Leu Asp Glu Leu Leu Asn Asn Ile  
 835 840 845  
 Ser Thr Ile Asn Thr Asp Leu Asp Ile Glu Ala Ser Gly Gly Tyr Asp  
 850 855 860  
 Asp Asp Leu Ile Ala Arg Leu Leu Lys Leu Gly Cys Cys Lys Asn Lys  
 865 870 875 880  
 Glu Ile Ala Val Lys Thr Val Lys Thr Ile Lys Phe Leu Gly Leu His  
 885 890 895  
 Glu Glu Thr Gln Ile Pro Lys Gly Cys Ser Ser Pro Phe Asp Val Ile  
 900 905 910  
 Cys Gln Arg Met Glu Gln Arg Met Ala Tyr Gly His Asn Glu Gln Asp  
 915 920 925  
 Met Val Leu Leu His His Glu Val Glu Val Glu Tyr Pro Asp Gly Gln  
 930 935 940



Pro Ala Glu Lys His Gln Ala Thr Leu Leu Glu Phe Gly Lys Val Glu  
 945 950 955 960  
 Asn Gly Arg Ser Thr Thr Ala Met Ala Leu Thr Val Gly Ile Pro Ala  
 965 970 975  
 Ala Ile Gly Ala Leu Leu Leu Leu Lys Asn Lys Val Gln Thr Lys Gly  
 980 985 990  
 Val Ile Arg Pro Leu Gln Pro Glu Ile Tyr Val Pro Ala Leu Glu Ile  
 995 1000 1005  
 Leu Glu Ser Ser Gly Ile Lys Leu Val Glu Lys Val Glu Thr  
 1010 1015 1020

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1908 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Zea mays

(ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 3..1908

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

ATTGTGCCCCG CCTTCTGCTA GGAGGAGGCA AGAACGGACC TCGAGTAAAC CGGATTATTG	60
TGCAGCCAAG CACAAGGAGG ATCCATCATG ACGCTCAGTA TGAGGATGCA GGATGCGAGA	120
TTTCAGAAGA CCTGTCAGAA TCGGCGCTTA TCATAGGCAT CAAACAACCC AAGCTGCAGA	180
TGATTCTTTC AGATAGAGCG TACGCTTTCT TTTACACAC ACACAAAGCC CAAAAGAGA	240
ATATGCCACT GTTAGACAAG ATCCTTGAAG AAAGGGTGTC CTTGTTTGAT TATGAGCTAA	300
TTGTTGGAGA TGATGGGAAA AGATCACTAG CATTTGGGAA ATTTGCTGGT AGAGCTGGAC	360
TGATAGATTT CTTACATGGT CTCGGACAGC GATATTTGAG CCTTGGATAC TCGACTCCAT	420
TTCTCTCTCT GGGACAATCT CATATGTATC CTTGCTCGC TGCAGCCAAG GCTGCAGTCA	480
TTGTGCTTGC AGAAGAGATA GCAACATTTG GACTTCCATC CGGAATTTGT CCGATAGTGT	540
TTGTGTTTAC TGGAGTTGGA AACGTCTCTC AGGGTGCGCA GGAGATATTC AAGTTATTGC	600
CCCATACCTT TGTTGATGCT GAGAAGCTTC CCGAAATTTT TCAGGCCAGG AATCTGTCTA	660
AGCAATCTCA GTCGACCAAG AGAGTATTTT AACTTTATGG TTGTGTTGTG ACCTCTAGAG	720
ACATAGTTTC TCACAAGGAT CCCACCAGAC AATTTGACAA AGGTGACTAT TATGCTCATC	780

CAGAACACTA CACCCCTGTT TTTCATGAAA GAATTGCTCC ATATGCATCT GTCATCGTAA 840  
 ACTGTATGTA TTGGGAGAAG AGGTTTCCAC CATTACTAAA TATGGATCAG TTACAGCAAT 900  
 TGATGGAGAC TGGTTGTCCT TTAGTCGGCG TTTGTGACAT AACTTGTGAT ATTGGAGGTT 960  
 CCATTGAATT TATCAACAAG AGTACATCAA TAGAGAGGCC TTTCTTTTCGG TATGATCCTT 1020  
 CTAAGAATTC ATACCATGAT GATATGGAAG GTGCCGGAGT GGTCTGCTTG GCTGTTGACA 1080  
 TTCTCCCTAC AGAATTCTCT AAAGAGGCCT CCCAACATTT TGGAAACATA CTATCTAGAC 1140  
 TTGTTGCTAG TTTGGCCTCA GTGAAGCAAC CGGCAGAACT TCCTTCCTAC TTGAGAAGAG 1200  
 CTTGCATTGC ACATGCTGGC AGATTAACTC CTTTGTATGA ATATATCCCT AGGATGAGAA 1260  
 ATACTATGAT AGATTTGGCA CCCGCAAAAA CAAATCCATT GCCTGACAAG AAGTATAGCA 1320  
 CCCTGGTATC TCTCAGTGGG CACCTATTTG ATAAGTTCCT TATAAATGAA GCTTTGGACA 1380  
 TCATTGAGAC AGCTGGAGGT TCATTTCACT TGGTTAGATG TGAAGTTGGA CAAAGCACGG 1440  
 ATGATATGTC ATACTCAGAG CTTGAAGTAG GAGCAGATGA TACTGCCACA TTGGATAAAA 1500  
 TTATTGATTC CTTGACTTCT TTAGCTAATG AACATGGTGG AGATCACGAT GCCGGGCAAG 1560  
 AAATTGAATT AGCTCTGAAG ATAGGAAAAG TCAATGAGTA TGAAACTGAC GTCACAATTG 1620  
 ATAAAGGAGG GCCAAAGATT TTAATTCTTG GAGCTGGAAG AGTCTGTCGG CCAGCTGCTG 1680  
 AGTTTCTGGC ATCTTACCCA GACATATGTA CCTATGGTGT TGATGACCAT GATGCAGATC 1740  
 AAATTCATGT TATCGTGGCA TCTTTGTATC AAAAAGATGC AGAAGAGACA GTTGATGGTA 1800  
 TTGAAAATAC AACTGCTACC CAGCTTGATG TTGCTGATAT TGGAAGCCTT TCAGATCTTG 1860  
 TTTCTCAGGT TGAGGTTGTA ATTAGCTTGC TGCCTGCTAG TTTTCATG 1908

(2) INFORMATION FOR SEQ ID NO:124:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 640 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 

- (A) ORGANISM: Zea mays

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

Cys	Ala	Arg	Leu	Leu	Leu	Gly	Gly	Gly	Lys	Asn	Gly	Pro	Arg	Val	Asn
1				5					10					15	
Arg	Ile	Ile	Val	Gln	Pro	Ser	Thr	Arg	Arg	Ile	His	His	Asp	Ala	Gln
			20					25					30		

Tyr Glu Asp Ala Gly Cys Glu Ile Ser Glu Asp Leu Ser Glu Cys Gly  
 35 40 45  
 Leu Ile Ile Gly Ile Lys Gln Pro Lys Leu Gln Met Ile Leu Ser Asp  
 50 55 60  
 Arg Ala Tyr Ala Phe Phe Ser His Thr His Lys Ala Gln Lys Glu Asn  
 65 70 75 80  
 Met Pro Leu Leu Asp Lys Ile Leu Glu Glu Arg Val Ser Leu Phe Asp  
 85 90 95  
 Tyr Glu Leu Ile Val Gly Asp Asp Gly Lys Arg Ser Leu Ala Phe Gly  
 100 105 110  
 Lys Phe Ala Gly Arg Ala Gly Leu Ile Asp Phe Leu His Gly Leu Gly  
 115 120 125  
 Gln Arg Tyr Leu Ser Leu Gly Tyr Ser Thr Pro Phe Leu Ser Leu Gly  
 130 135 140  
 Gln Ser His Met Tyr Pro Ser Leu Ala Ala Ala Lys Ala Ala Val Ile  
 145 150 155 160  
 Val Val Ala Glu Glu Ile Ala Thr Phe Gly Leu Pro Ser Gly Ile Cys  
 165 170 175  
 Pro Ile Val Phe Val Phe Thr Gly Val Gly Asn Val Ser Gln Gly Ala  
 180 185 190  
 Gln Glu Ile Phe Lys Leu Leu Pro His Thr Phe Val Asp Ala Glu Lys  
 195 200 205  
 Leu Pro Glu Ile Phe Gln Ala Arg Asn Leu Ser Lys Gln Ser Gln Ser  
 210 215 220  
 Thr Lys Arg Val Phe Gln Leu Tyr Gly Cys Val Val Thr Ser Arg Asp  
 225 230 235 240  
 Ile Val Ser His Lys Asp Pro Thr Arg Gln Phe Asp Lys Gly Asp Tyr  
 245 250 255  
 Tyr Ala His Pro Glu His Tyr Thr Pro Val Phe His Glu Arg Ile Ala  
 260 265 270  
 Pro Tyr Ala Ser Val Ile Val Asn Cys Met Tyr Trp Glu Lys Arg Phe  
 275 280 285  
 Pro Pro Leu Leu Asn Met Asp Gln Leu Gln Gln Leu Met Glu Thr Gly  
 290 295 300  
 Cys Pro Leu Val Gly Val Cys Asp Ile Thr Cys Asp Ile Gly Gly Ser  
 305 310 315 320  
 Ile Glu Phe Ile Asn Lys Ser Thr Ser Ile Glu Arg Pro Phe Phe Arg  
 325 330 335  
 Tyr Asp Pro Ser Lys Asn Ser Tyr His Asp Asp Met Glu Gly Ala Gly  
 340 345 350  
 Val Val Cys Leu Ala Val Asp Ile Leu Pro Thr Glu Phe Ser Lys Glu  
 355 360 365  
 Ala Ser Gln His Phe Gly Asn Ile Leu Ser Arg Leu Val Ala Ser Leu  
 370 375 380

Ala Ser Val Lys Gln Pro Ala Glu Leu Pro Ser Tyr Leu Arg Arg Ala  
 385 390 395 400  
 Cys Ile Ala His Ala Gly Arg Leu Thr Pro Leu Tyr Glu Tyr Ile Pro  
 405 410 415  
 Arg Met Arg Asn Thr Met Ile Asp Leu Ala Pro Ala Lys Thr Asn Pro  
 420 425 430  
 Leu Pro Asp Lys Lys Tyr Ser Thr Leu Val Ser Leu Ser Gly His Leu  
 435 440 445  
 Phe Asp Lys Phe Leu Ile Asn Glu Ala Leu Asp Ile Ile Glu Thr Ala  
 450 455 460  
 Gly Gly Ser Phe His Leu Val Arg Cys Glu Val Gly Gln Ser Thr Asp  
 465 470 475 480  
 Asp Met Ser Tyr Ser Glu Leu Glu Val Gly Ala Asp Asp Thr Ala Thr  
 485 490 495  
 Leu Asp Lys Ile Ile Asp Ser Leu Thr Ser Leu Ala Asn Glu His Gly  
 500 505 510  
 Gly Asp His Asp Ala Gly Gln Glu Ile Glu Leu Ala Leu Lys Ile Gly  
 515 520 525  
 Lys Val Asn Glu Tyr Glu Thr Asp Val Thr Ile Asp Lys Gly Gly Pro  
 530 535 540  
 Lys Ile Leu Ile Leu Gly Ala Gly Arg Val Cys Arg Pro Ala Ala Glu  
 545 550 555 560  
 Phe Leu Ala Ser Tyr Pro Asp Ile Cys Thr Tyr Gly Val Asp Asp His  
 565 570 575  
 Asp Ala Asp Gln Ile His Val Ile Val Ala Ser Leu Tyr Gln Lys Asp  
 580 585 590  
 Ala Glu Glu Thr Val Asp Gly Ile Glu Asn Thr Thr Ala Thr Gln Leu  
 595 600 605  
 Asp Val Ala Asp Ile Gly Ser Leu Ser Asp Leu Val Ser Gln Val Glu  
 610 615 620  
 Val Val Ile Ser Leu Leu Pro Ala Ser Phe His Ala Ala Ile Ala Gly  
 625 630 635 640

(2) INFORMATION FOR SEQ ID NO:125:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 720 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: *Oryza sativa*

- (ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 2..720
- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 215  
 (D) OTHER INFORMATION: /label= unknown
- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 678  
 (D) OTHER INFORMATION: /label= unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

```

GTTTAAACAT CTTTCCAATC TTGTTTCTCA GGTGAAGTA GTAGTTAGCT TGCTGCCTGC      60
CAGTTTTTCAT GCTGCCATAG CAAGAGTATG CATAGAGATG AAGAAGCACT TGGTCACTGC    120
AAGCTATGTT GATGAGTCCA TGTCAAAGTT GGAACAATCT GCAGAAGGTG CTGGTGTAAC    180
TATTCTCTGT GAAATGGGCC TGGATCCTGG CATANATCAT ATGATGTCAA TGAAGATGAT    240
TGACGAAGCA CATTACGGA AGGGGAAAAT AAAGTCATTT ACATCCTTTT GTGGAGGACT      300
TCCATCTCCA GCTTCTGCAA ACAATCCACT TGCTTATAAG TTCAGTTGGA GTCCAGCTGG     360
TGCCATCCGT GCAGGGAGAA ACCCTGCTGT CTACAAATTT CATGGAGAAA TCATCCATGT     420
AGATGGTGAT AAATTGTATG AATCCGCAAA GAGGCTCAGA TTACMAGAAC TTCCAGCTTT     480
TGCACTGGAA CACTTGCCAA ACCGGAATTC CTTGATGTAT GGAGACCTGT ATGGGATCTC    540
CAAAGAAGCA TCTACTGTGT ACAGGGCTAC TCTTCGTTAT GAAGGATTTA ATGAGATAAT    600
GGCAACCTTC GCGAAAATTG GGTTTTTTGA TGCTGCAAGT CATCCACTGT TGCAACAAAC     660
TACTCGCCCT ACATACANGG ATTCCTGTG GAACCCTCAA TGCTGTACA TCTCCAAAAC      720
  
```

(2) INFORMATION FOR SEQ ID NO:126:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 239 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: *Oryza sativa*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

```

Phe Lys His Leu Ser Asn Leu Val Ser Gln Val Glu Val Val Val Ser
1           5           10           15
Leu Leu Pro Ala Ser Phe His Ala Ala Ile Ala Arg Val Cys Ile Glu
  
```

20										25										30																																		
Met	Lys	Lys	His	Leu	Val	Thr	Ala	Ser	Tyr	Val	Asp	Glu	Ser	Met	Ser																																							
		35					40					45																																										
Lys	Leu	Glu	Gln	Ser	Ala	Glu	Gly	Ala	Gly	Val	Thr	Ile	Leu	Cys	Glu																																							
	50					55					60																																											
Met	Gly	Leu	Asp	Pro	Gly	Ile	Xaa	His	Met	Met	Ser	Met	Lys	Met	Ile																																							
65					70				75						80																																							
Asp	Glu	Ala	His	Ser	Arg	Lys	Gly	Lys	Ile	Lys	Ser	Phe	Thr	Ser	Phe																																							
				85					90						95																																							
Cys	Gly	Gly	Leu	Pro	Ser	Pro	Ala	Ser	Ala	Asn	Asn	Pro	Leu	Ala	Tyr																																							
			100					105					110																																									
Lys	Phe	Ser	Trp	Ser	Pro	Ala	Gly	Ala	Ile	Arg	Ala	Gly	Arg	Asn	Pro																																							
		115					120					125																																										
Ala	Val	Tyr	Lys	Phe	His	Gly	Glu	Ile	Ile	His	Val	Asp	Gly	Asp	Lys																																							
	130					135					140																																											
Leu	Tyr	Glu	Ser	Ala	Lys	Arg	Leu	Arg	Leu	Xaa	Glu	Leu	Pro	Ala	Phe																																							
145					150				155						160																																							
Ala	Leu	Glu	His	Leu	Pro	Asn	Arg	Asn	Ser	Leu	Met	Tyr	Gly	Asp	Leu																																							
				165				170							175																																							
Tyr	Gly	Ile	Ser	Lys	Glu	Ala	Ser	Thr	Val	Tyr	Arg	Ala	Thr	Leu	Arg																																							
			180					185					190																																									
Tyr	Glu	Gly	Phe	Asn	Glu	Ile	Met	Ala	Thr	Phe	Ala	Lys	Ile	Gly	Phe																																							
		195					200					205																																										
Phe	Asp	Ala	Ala	Ser	His	Pro	Leu	Leu	Gln	Gln	Thr	Thr	Arg	Pro	Thr																																							
	210					215					220																																											
Tyr	Xaa	Asp	Phe	Leu	Leu	Asn	Pro	Gln	Cys	Leu	Tyr	Ile	Ser	Lys																																								
225					230				235																																													

(2) INFORMATION FOR SEQ ID NO:127:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 308 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: *Oryza sativa*
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 1..129
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

CTGCTGTTGC TCCAGAACAA GATCCAAAAG AAAGGAGTGA TCAGGCCTCT GGAACCTGAA 60  
 ATTTACATTC CAGCGTTGGA GATCTTGGAG TCATCGGGTA TCAAGCTGGC GGAGAGAGTG 120  
 GAGACCTGAG AATCGGACCC AATATGTATA ATGTAGCATG GTGGTAGCTT CTCTATATAT 180  
 ATGCTTCAGT GAATAATTGA TTTGCCGTTG TGTGGTAATT AAGCAATGCC CGCTAATAAA 240  
 TTGTACCGTA GAAGTCCTTC TATGTACATC CGTATCAAAA AATAAAAAAA GCATCGATTA 300  
 GCTTGAAT 308

(2) INFORMATION FOR SEQ ID NO:128:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 42 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 

- (A) ORGANISM: *Oryza sativa*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

Leu	Leu	Leu	Leu	Gln	Asn	Lys	Ile	Gln	Lys	Lys	Gly	Val	Ile	Arg	Pro
1				5					10					15	
Leu	Glu	Pro	Glu	Ile	Tyr	Ile	Pro	Ala	Leu	Glu	Ile	Leu	Glu	Ser	Ser
			20					25					30		
Gly	Ile	Lys	Leu	Ala	Glu	Arg	Val	Glu	Thr						
		35					40								

(2) INFORMATION FOR SEQ ID NO:129:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 429 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 

- (A) ORGANISM: *Triticum aestivum*

(ix) FEATURE:
 

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..252

(ix) FEATURE:
 

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 172

(D) OTHER INFORMATION: /label= unknown

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION: 186

(D) OTHER INFORMATION: /label= unknown

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION: 331

(D) OTHER INFORMATION: /label= unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

```
TACCCCGACG GGGACCCAC CGAGAAGCAC CAAGCGACGC TGCTGGAGTT CGGAAAGACC      60
GAGAACGGCA GGCCCACCAC CGCCATGGCC CTCACCGTTG GGGTACCGGC AGCGATAGGA      120
GCCCTGCTCT TGCTCCAGAA CAAGGTCCAG AGGAAAGGGG TGATCCGGCC TNTGGAACCG      180
GAGATNTACA TCCCTGCGCT GGAGATCTTG GAAGCGTCGG GCATCAAGCT GATCGAGAGA      240
GTGGAGACCT GAGGATGTCA GGATGGGATG AGAATCTATC GAGTATATAT GCTGCAGCAA      300
CAGAGGCAGT GAGTAAATAA AATGATGATT NTCGCCGTTG TAAGTAAAT GAGTGGACTG      360
TATGTATGTA TGTGACTATC TATTGTACTA CATATATACC AAATCTGTCT CCGGTTGATT      420
CTGTTGGTG                                     429
```

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 83 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Triticum aestivum

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

```
Tyr Pro Asp Gly Asp Pro Thr Glu Lys His Gln Ala Thr Leu Leu Glu
1           5           10           15
Phe Gly Lys Thr Glu Asn Gly Arg Pro Thr Thr Ala Met Ala Leu Thr
20           25           30
Val Gly Val Pro Ala Ala Ile Gly Ala Leu Leu Leu Leu Gln Asn Lys
35           40           45
Val Gln Arg Lys Gly Val Ile Arg Pro Xaa Glu Pro Glu Xaa Tyr Ile
50           55           60
Pro Ala Leu Glu Ile Leu Glu Ala Ser Gly Ile Lys Leu Ile Glu Arg
65           70           75           80
```



Val Glu Thr

(2) INFORMATION FOR SEQ ID NO:131:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1449 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

```
ATGACGAAAA AATCAGGTGT TTGATTCTT GGTGCTGGAC GTGTGTGTCTG CCCAGCTGCT      60
GATTTCTTAG CTTCAGTTAG AACCATTTCG TCACAGCAAT GGTACAAAAC ATATTTTCGGA      120
GCAGACTCTG AAGAGAAAAC AGATGTTTCTG GTGATTGTCTG CGTCTCTGTA TCTTAAGGAT      180
GCCAAAGAGA CGGTTGAAGG TATTTTCAGAT GTAGAAGCAG TTCGGCTAGA TGTATCTGAT      240
AGTGAAAGTC TCCTTAAGTA TGTTTCTCAG GTTGATGTTG TCCTAAGTTT ATTACCTGCA      300
AGTTGTCATG CTGTTGTAGC AAAGACATGC ATTGAGCTGA AGAAGCATCT CGTCACTGCT      360
AGCTATGTTG ATGATGAAAC GTCCATGTTA CATGAGAAGG CTAAGAGTGC TGGGATAACG      420
ATTCTAGGCG AAATGGGACT GGACCCTGGA ATCGATCACA TGATGGCGAT GAAAATGATC      480
AACGATGCTC ATATCAAAAA AGGGAAAAGTG AAGTCTTTTA CCTCTTATTG TGGAGGGCTT      540
CCCTCTCCTG CTGCAGCAAA TAATCCATTA GCATATAAAT TTAGCTGGAA CCCTGCTGGA      600
GCAATTCGAG CTGGTCAAAA CCCCGCCAAA TACAAAAGCA ACGGCGACAT AATACATGTT      660
GATGGGAAGA ATCTCTATGA TTCCGCGGCA AGATTCCGAG TACCTAATCT TCCAGCTTTT      720
GCATTGGAGT GTTTTCCAAA TCGTGACTCC TTGGTTTACG GGGAACATTA TGGCATCGAG      780
AGCGAAGCAA CAACGATATT TCGTGGAACA CTCAGATATG AAGGGTTTAG TATGATAATG      840
GCAACACTTT CGAAACTTGG ATTCTTTGAC AGTGAAGCAA ATCAAGTACT CTCCACTGGA      900
AAGAGGATTA CGTTTGGTGC TCTTTTAAGT AACATTCTAA ATAAGGATGC AGACAATGAA      960
TCAGAGCCCC TAGCGGGAGA AGAAGAGATA AGCAAGAGAA TTATCAAGCT TGGACATTCC     1020
AAGGAGACTG CAGCCAAAGC TGCCAAAACA ATTGTATTCT TGGGGTTCAA CGAAGAGAGG     1080
GAGGTTCCAT CACTGTGTAA AAGCGTATTT GATGCAACTT GTTACCTAAT GGAAGAGAAA     1140
CTAGCTTATT CCGGAAATGA ACAGGACATG GTGCTTTTGC ATCACGAAGT AGAAGTGGAA     1200
TTCCTTGAAA GCAAACGTAT AGAGAAGCAC ACTGCGACTC TTTTGGAATT CGGGGACATC     1260
AAGAATGGAC AAACAACAAC CGCTATGGCC AAGACTGTTG GGATCCCTGC AGCCATTGGA     1320
```

GCTCTGGTGT TAATTGAAGA CAAGATCAAG ACAAGAGGAG TCTTAAGGCC TCTCGAAGCA 1380  
 GAGGTGTATT TGCCAGCTTT GGATATATTG CAAGCATATG GTATAAAGCT GATGGAGAAG 1440  
 GCAGAATGA 1449

(2) INFORMATION FOR SEQ ID NO:132:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 482 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: unknown  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

Met	Thr	Lys	Lys	Ser	Gly	Val	Leu	Ile	Leu	Gly	Ala	Gly	Arg	Val	Cys	1	5	10	15
Arg	Pro	Ala	Ala	Asp	Phe	Leu	Ala	Ser	Val	Arg	Thr	Ile	Ser	Ser	Gln	20	25	30	
Gln	Trp	Tyr	Lys	Thr	Tyr	Phe	Gly	Ala	Asp	Ser	Glu	Glu	Lys	Thr	Asp	35	40	45	
Val	His	Val	Ile	Val	Ala	Ser	Leu	Tyr	Leu	Lys	Asp	Ala	Lys	Glu	Thr	50	55	60	
Val	Glu	Gly	Ile	Ser	Asp	Val	Glu	Ala	Val	Arg	Leu	Asp	Val	Ser	Asp	65	70	75	80
Ser	Glu	Ser	Leu	Leu	Lys	Tyr	Val	Ser	Gln	Val	Asp	Val	Val	Leu	Ser	85	90	95	
Leu	Leu	Pro	Ala	Ser	Cys	His	Ala	Val	Val	Ala	Lys	Thr	Cys	Ile	Glu	100	105	110	
Leu	Lys	Lys	His	Leu	Val	Thr	Ala	Ser	Tyr	Val	Asp	Asp	Glu	Thr	Ser	115	120	125	
Met	Leu	His	Glu	Lys	Ala	Lys	Ser	Ala	Gly	Ile	Thr	Ile	Leu	Gly	Glu	130	135	140	
Met	Gly	Leu	Asp	Pro	Gly	Ile	Asp	His	Met	Met	Ala	Met	Lys	Met	Ile	145	150	155	160
Asn	Asp	Ala	His	Ile	Lys	Lys	Gly	Lys	Val	Lys	Ser	Phe	Thr	Ser	Tyr	165	170	175	
Cys	Gly	Gly	Leu	Pro	Ser	Pro	Ala	Ala	Ala	Asn	Asn	Pro	Leu	Ala	Tyr	180	185	190	
Lys	Phe	Ser	Trp	Asn	Pro	Ala	Gly	Ala	Ile	Arg	Ala	Gly	Gln	Asn	Pro	195	200	205	

Ala Lys Tyr Lys Ser Asn Gly Asp Ile Ile His Val Asp Gly Lys Asn  
 210 215 220  
 Leu Tyr Asp Ser Ala Ala Arg Phe Arg Val Pro Asn Leu Pro Ala Phe  
 225 230 235 240  
 Ala Leu Glu Cys Phe Pro Asn Arg Asp Ser Leu Val Tyr Gly Glu His  
 245 250 255  
 Tyr Gly Ile Glu Ser Glu Ala Thr Thr Ile Phe Arg Gly Thr Leu Arg  
 260 265 270  
 Tyr Glu Gly Phe Ser Met Ile Met Ala Thr Leu Ser Lys Leu Gly Phe  
 275 280 285  
 Phe Asp Ser Glu Ala Asn Gln Val Leu Ser Thr Gly Lys Arg Ile Thr  
 290 295 300  
 Phe Gly Ala Leu Leu Ser Asn Ile Leu Asn Lys Asp Ala Asp Asn Glu  
 305 310 315 320  
 Ser Glu Pro Leu Ala Gly Glu Glu Glu Ile Ser Lys Arg Ile Ile Lys  
 325 330 335  
 Leu Gly His Ser Lys Glu Thr Ala Ala Lys Ala Ala Lys Thr Ile Val  
 340 345 350  
 Phe Leu Gly Phe Asn Glu Glu Arg Glu Val Pro Ser Leu Cys Lys Ser  
 355 360 365  
 Val Phe Asp Ala Thr Cys Tyr Leu Met Glu Glu Lys Leu Ala Tyr Ser  
 370 375 380  
 Gly Asn Glu Gln Asp Met Val Leu Leu His His Glu Val Glu Val Glu  
 385 390 395 400  
 Phe Leu Glu Ser Lys Arg Ile Glu Lys His Thr Ala Thr Leu Leu Glu  
 405 410 415  
 Phe Gly Asp Ile Lys Asn Gly Gln Thr Thr Thr Ala Met Ala Lys Thr  
 420 425 430  
 Val Gly Ile Pro Ala Ala Ile Gly Ala Leu Val Leu Ile Glu Asp Lys  
 435 440 445  
 Ile Lys Thr Arg Gly Val Leu Arg Pro Leu Glu Ala Glu Val Tyr Leu  
 450 455 460  
 Pro Ala Leu Asp Ile Leu Gln Ala Tyr Gly Ile Lys Leu Met Glu Lys  
 465 470 475 480  
 Ala Glu